

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:43:51 ; Search time 166 Seconds
(without alignments)
866.716 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPLTLENDLENLEDFWE.....PSWRSSLSSENAISLTTF 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003s:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1953	100.0	372	2	AAR27793 New plate
2	1953	100.0	372	2	AAR68813 Human lym
3	1953	100.0	372	2	AAR92239 Chemokine
4	1953	100.0	372	2	AAY06644 Human Bur
5	1953	100.0	372	3	AAY90627 Human G p
6	1953	100.0	372	4	AAG80124 Human CX
7	1953	100.0	372	6	ABP81789 Human CX
8	1953	100.0	372	7	ADC22585 Human G p
9	1953	100.0	372	8	ADH14058 Human BLR
10	1953	100.0	372	8	ADJ45761 Human CX
11	1953	100.0	372	8	ADO29199 Human GPC
12	1953	100.0	372	8	ADR66972 Human can
13	1953	100.0	378	4	ABB11873 Human Bur
14	1947	99.7	372	3	AAY90661 Human mut
15	1947	99.7	372	7	ADC22719 Human G p
16	1947	99.7	372	7	ADH14192 Mutated h
17	1638	83.9	374	8	ADR66969 Mouse can
18	1635	83.7	374	2	AAY06643 Mouse Bur
19	1635	83.7	374	8	ADO29200 Mouse GPC
20	1470	75.3	741	4	ABG19581 Novel hum
21	635	32.5	368	2	AAY54371 Human IP-
22	635	32.5	368	3	AAY90614 Human G p
23	635	32.5	368	4	AAG80122 Human CX
24	635	32.5	368	6	ABP81795 Human CX
25	635	32.5	368	7	AAC38602 Human C-X

26	635	32.5	368	7	ADC22539	Adc22539 Human G p
27	635	32.5	368	7	ADF17988	Adf17988 Human CX
28	635	32.5	368	7	ADH14012	Adh14012 Human GPR
29	635	32.5	368	7	ADN39434	Adn39434 Cancer/an
30	635	32.5	368	8	ADH61810	Adh61810 Human G p
31	635	32.5	368	8	ADO29458	Ado29458 Human GPC
32	635	32.5	368	8	ADP12496	Adp12496 Protein e
33	635	32.5	368	8	ADP12922	Adp12922 Protein e
34	635	32.5	368	8	ADQ09119	Adq09119 Human CX
35	635	32.5	368	8	ADQ59336	Adq59336 T cell ac
36	635	32.5	368	8	ADR67008	Adr67008 Human can
37	635	32.5	368	8	ADS73812	Ads73812 Human CX
38	635	32.5	378	2	AAY50129	Aay50129 Human che
39	635	32.5	415	7	ADC46963	Adc46963 Human CX
40	635	32.5	415	8	ADH61808	Adh61808 Human G p
41	634	32.4	415	8	ADQ95988	Adq95988 T cell ac
42	632	32.4	368	3	AAY90648	Aay90648 Human mut
43	632	32.4	368	7	ADC22693	Adc22693 Human G p
44	632	32.4	368	7	ADH14166	Adh14166 Mutated h
45	630	32.3	368	8	ADS73816	Ads73816 Human non

ALIGNMENTS

RESULT 1
AAR27793
ID AAR27793 standard; protein; 372 AA.
XX
AC AAR27793;
XX
DT 25-MAR-2003 (revised)
DT 12-MAR-1993 (first entry)
XX
DE New platelet factor 4 receptor superfamily member PF4ARii.
XX
KW IL-8R; G-protein coupled receptor family; rhodopsin superfamily;
KW pro-inflammatory cytokine; 8rr.9.
XX
OS Homo sapiens.
XX
PN WO9217497-A1.
XX
PD 15-OCT-1992.
XX
PF 23-MAR-1992; 92WO-US002317.
XX
PR 29-MAR-1991; 91US-00677211.
PR 19-DEC-1991; 91US-00810782.
XX
(GETH) GENENTECH INC.
XX
PI Lee J, Holmes WE, Wood WI;
XX
WPI; 1992-366191/44.
XX
N-PSDB; AAQ37107.
XX
Isolated human platelet factor 4 super-family receptor polypeptide and
corresp. antibodies and DNA - useful as diagnostic and screening agents,
and for treating inflammation or PF4AR-mediated disorders.
XX
Claim 7; Fig 5; 78pp; English.
XX
The IL-8 receptor cDNA sequence was isolated (see AAO29505) and a 874bp
sub-fragment of the coding sequence was used as a probe to screen human
cell line HL60 and human peripheral blood lymphocyte cDNA libraries. Two
new gene sequences were found that are clearly related to the IL-8
receptor. One of these was contained in clone 8rr.9 and is predicted to
encode an amino acid sequence which is 36% and 38% identical with the
high and low affinity IL-8 receptor sequences, respectively. See also
AAQ37107. (Updated on 25-MAR-2003 to correct FN field.)
XX
Sequence 372 AA;
SQ

Query Match 100.0%; Score 1953; DB 2; Length 372; Mismatches 0; Indels 0; Gaps 0; Best Local Similarity 100.0%; Pred. No. 1.8e-196; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60

QY 61 IFLGVGNVLVLILERHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWGLTF 120
DB 61 IFLGVGNVLVLILERHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWGLTF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHLRQAQRPRQOKAVRVAILVTSIFFLCWSPIHIVIFDLTLARLKAVDNTCKLNGSL 300
DB 241 VVHLRQAQRPRQOKAVRVAILVTSIFFLCWSPIHIVIFDLTLARLKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 2
AAR68813 standard; protein; 372 AA.
ID AAR68813
AC AAR68813;
XX
XX 25-MAR-2003 (revised)
DT 18-JUL-1995 (first entry)
DE Human lymphocyte PF4AR.
XX
XX Interleukin-8 receptor; IL-8 receptor; PF4AR;
KW platelet factor superfamily receptor; lymphocyte; chemotactic;
KW inflammation; inflammatory disease; arthritis; emphysema; cystic;
KW fibrosis; colitis; bronchitis; meningitis; therapeutic.
XX
XX Homo sapiens.
OS
XX WO9428931-A1.
PN
XX
XX 22-DEC-1994.
XX
XX 07-JUN-1994; 94WO-US006380.
XX
XX 11-JUN-1993; 93US-00076093.
PR
XX (GETH) GENENTECH INC.
XX
XX Chuntharapai A, Lee J, Hebert C, Kim KJ;
PI
XX WPI; 1995-036114/05.
DR N-PSDB; AAQ80522.
DR
XX Treatment of inflammatory disorders - by administering an antibody
PT capable of binding a platelet factor 4 superfamily receptor polypeptide.
PT
XX Disclosure; Page 56-58; 83pp; English.
PS
XX 2 PF4AR members were identified by probing lambda libraries from human
XX CC

CC monoclyte-like cell line HL-60 and human peripheral blood lymphocytes
CC using a large fragment of IL-8 receptor DNA (full sequence given in
CC AAQ80520). The nucleotide sequences of the 2 PF4ARs are given in AAQ80521
CC and AAQ80522, and their respective amino acid sequences in AAR68812 and
CC AAR68813. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 2; Length 372; Best Local Similarity 100.0%; Pred. No. 1.8e-196; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60

QY 61 IFLGVGNVLVLILERHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWGLTF 120
DB 61 IFLGVGNVLVLILERHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWGLTF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDYLAIVHAVHAYRHRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHLRQAQRPRQOKAVRVAILVTSIFFLCWSPIHIVIFDLTLARLKAVDNTCKLNGSL 300
DB 241 VVHLRQAQRPRQOKAVRVAILVTSIFFLCWSPIHIVIFDLTLARLKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 3
AAR92239 standard; protein; 372 AA.
ID AAR92239
AC AAR92239;
XX
XX 25-MAR-2003 (revised)
DT 26-MAR-1996 (first entry)
XX
XX Chemokine superfamily receptor.
XX
XX Interleukin; IL-8; inflammation; psoriasis; dermatitis;
KW rheumatoid arthritis; inflammatory bowel disease;
KW chronic lung inflammation; treatment; antibody; affinity purification;
KW detection.
XX
XX Homo sapiens.
OS
XX US5440021-A.
PN
XX 08-AUG-1995.
PD
XX 25-FEB-1994; 94US-00202056.
PF
XX 29-MAR-1991; 91US-00677211.
PR
XX (HEBE/) HEBERT C.
PA (CHUN/) CHUNTHARAPAI A.
PA (KIMK/) KIM K J.
PA (LEEJ/) LEE J.
XX
XX Chuntharapai A, Kim KJ, Hebert C, Lee J;
PI

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XX WPI; 1995-283151/37.
DR N-PSDB; AAQ99009.
XX
XX
XX New antibodies against interleukin 8 type B receptor - used to treat or
PT prevent inflammation, also for detecting receptor expression and
PT purificn.
XX
XX Example 2; Col 49-52; 62pp; English.
XX
XX Antibodies directed against the interleukin-8 receptor B can be used to
CC treat or prevent inflammation e.g. psoriasis, dermatitis, rheumatoid
CC arthritis and particularly inflammatory bowel disease and chronic lung
CC inflammation. When immobilised, these antibodies may be used to detect
CC interleukin-8 receptor B expression in cells and tissues and for affinity
CC purification of interleukin-8 receptor B from cells. This sequence is an
CC additional chemokine superfamily receptor which was identified by probing
CC lambda libraries of genomic DNA from a human monocyte-like cell line (L-
CC 60) and human peripheral blood lymphocytes using a large fragment of the
CC interleukin-8 type A receptor DNA (See AAQ99006). (Updated on 25-MAR-2003
CC to correct PF field.)
XX
XX Sequence 372 AA;
XX
Query Match      100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
RB 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
QY 61 IFLLGVIGNVLVILERHQRQTSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
DB 61 IFLLGVIGNVLVILERHQRQTSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLVMGVCY 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLVMGVCY 240
QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLPFSWRSS 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 4
AA06644
ID AA06644 standard; protein; 372 AA.
XX
AC AA06644;
XX
XX 26-OCT-1999 (first entry)
XX
XX Human Burkitt's lymphoma receptor 1 (BLR1).
XX
XX Burkitt's lymphoma receptor 1; BLR1; human; B lymphocyte chemoattractant;
XX BLC; chemokine; ligand; drug screening; leukaemia; autoimmune disease;
XX therapy.
XX
XX Homo sapiens.
XX

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PN WO9928468-A1.
XX
XX 10-JUN-1999.
XX
XX 02-DEC-1998; 98WO-US025561.
XX
XX 02-DEC-1997; 97US-00982493.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Gunn MD, Williams LT, Cyster JG;
XX
XX WPI; 1999-493764/41.
XX N-PSDB; AA087710.
XX
XX Modulating interaction of a Burkitt's Lymphoma Receptor 1 polypeptide and
PT ligand, useful in drug screens.
XX
XX Claim 1; Page 38; 42pp; English.
XX
XX This sequence represents human Burkitt's lymphoma receptor 1 (BLR1). The
CC invention relates to methods for modulating the interaction of BLR1 with
CC its ligand. B lymphocyte chemoattractant (BLC, see AA06642). The methods
CC comprise combining BLR1 and BLC polypeptides with a candidate modulator
CC agent under conditions whereby, but for the presence of the agent, the
CC polypeptides engage in a first interaction, and determining a second
CC interaction of the polypeptides in the presence of the agent, wherein a
CC difference between the first and second interactions indicates that the
CC agent modulates the interaction of the polypeptides. The modulator is
CC preferably an antagonist, especially dominant negative, form of BLC. BLC
CC and BLC agonists and antagonists may be useful for treating viral (e.g.
CC HIV) infections, lymphoma, B lineage leukaemia, and autoimmune diseases
CC such as rheumatoid arthritis, thyroiditis and diabetes
XX
XX Sequence 372 AA;
XX
Query Match      100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
QY 61 IFLLGVIGNVLVILERHQRQTSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
DB 61 IFLLGVIGNVLVILERHQRQTSSTETFLFLAVADLLVFLPFAVAEGSGVWLGT 120
QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAI VHAHVAYHRRLLSIHITCGTIWLVGFL 180
QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLVMGVCY 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHAGFLPMLVMGVCY 240
QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCQLPFSWRSS 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 5
AA06644
ID AA06644 standard; protein; 372 AA.
XX

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AC AAY90627;
 XX 21-AUG-2000 (first entry)
 XX Human G protein-coupled receptor BLR1.
 DE
 XX G protein-coupled receptor; GPCR; constitutively active;
 KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;
 KW antagonist.
 XX
 XX Homo sapiens.
 OS
 XX W0200022129-A1.
 PN
 XX 20-APR-2000.
 XX
 XX 12-OCT-1999; 99WO-US023938.
 PF
 XX 13-OCT-1998; 98US-00170496.
 PR
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Behan DP, Chalmers DT, Liaw CW;
 PI
 XX WPI; 2000-329165/28.
 DR
 DR N-PSDB; AAA30626.
 XX
 XX Non-endogenous constitutively activated human G protein-coupled
 PT receptors, useful for identifying agonists for use as pharmaceutical
 PT agents.
 PT
 XX
 XX Example 1; Page 152-153; 341pp; English.
 PS
 XX The invention relates to constitutively active, non-endogenous versions
 CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
 CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
 CC and AAA30775-A30779). The mutant proteins of the invention contain a
 CC mutation in a portion of the protein comprising intracellular loop 3
 CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
 CC is substituted for an endogenous residue in IC3 at a position 16 amino
 CC acids N-terminal of an endogenous residue in TM6 to form a sequence X-
 CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
 CC Ala, and is preferably Lys. When the endogenous residue at this position
 CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
 CC amino acid stretch between the substituted amino acid and the pro may be
 CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
 CC residues. The constitutively active GPCRs are useful for identifying
 CC antagonists, agonists and partial agonists for use as pharmaceutical
 CC agents. The mutant proteins are also useful in research settings for
 CC elucidating the roles of the receptors in normal and diseased conditions.
 CC Antagonists for a particular GPCR are useful for treating diseases and
 CC disorders associated with that receptor. Because the novel mutant GPCRs
 CC are constitutively active, they can be used directly for screening of
 CC compounds without the need for endogenous ligands. The present sequence
 CC represents a human wild-type GPCR referred to in an exemplification of
 CC the invention
 XX
 XX Sequence 372 AA;
 SQ
 Query Match 100.0%; Score 1953; DB 3; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
 DB 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYS 60
 QY 61 IFLLGVIGNVLVILRRHRQTRSSSTTFFLHLAVADLLVFLPFAVAGSGVGVLTGF 120
 DB 61 IFLLGVIGNVLVILRRHRQTRSSSTTFFLHLAVADLLVFLPFAVAGSGVGVLTGF 120
 QY 121 LCKTVIALHKVNFYCSSLLACIADVRYLAIVHAVHAYRHRLLSHITCGTILWVGFL 180

DB 121 LCKTVIALHKVNFYCSSLLACIADVRYLAIVHAVHAYRHRLLSHITCGTILWVGFL 180
 QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
 DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
 QY 241 VVHRLRQARRPQOROKAVRVAILVTSIFPLCWSPHIVIFLDTLRLKAVDNTCKLNGSL 300
 DB 241 VVHRLRQARRPQOROKAVRVAILVTSIFPLCWSPHIVIFLDTLRLKAVDNTCKLNGSL 300
 QY 301 PVAITWCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPSPWRRSSL 360
 DB 301 PVAITWCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPSPWRRSSL 360
 QY 361 SESENATSLTTF 372
 DB 361 SESENATSLTTF 372
 RESULT 6
 AAG80124
 ID AAG80124 standard; protein; 372 AA.
 XX
 AC AAG80124;
 XX
 DT 17-JAN-2002 (first entry)
 XX
 DE Human CXCR5 protein.
 XX
 KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
 KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
 KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
 KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
 KW antirheumatic; antiarthritic.
 XX
 OS Homo sapiens.
 OS
 PN W0200172830-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 02-APR-2001; 2001WO-EP003708.
 PR
 PR 31-MAR-2000; 2000DE-01016013.
 XX
 XX (IPFP-) IPF PHARM GMBH.
 PA (FORS/) FORSSMANN U.
 PA
 PI Forssmann W, Adermann K, Heitland A, Spodeberg N;
 XX
 DR WPI; 2001-626256/72.
 XX
 PT Diagnostic agent containing two or more receptor-specific ligands, useful
 PT for detecting tumors, inflammation etc., also therapeutic use of ligand
 PT inhibitors.
 XX
 PS Disclosure; Page 12-13; 26pp; German.
 XX
 CC This invention describes a novel diagnostic agent (A) comprising at least
 CC two different ligands (I) for receptors (II) that are implicated in
 CC disease. (A) are used for the diagnosis of tumors (especially colorectal
 CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (I) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antiasthmatic,
 CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
 CC Chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine

CC fragments used to illustrate the method of the invention
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYSL 60

QY 61 IFLGVGNVLVILVILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
DB 61 IFLGVGNVLVILVILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAIVHAYHRRLLSIHITCGTILVGFLL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAIVHAYHRRLLSIHITCGTILVGFLL 180

QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAMFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAMFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLNCSPYHIVIFDLTLARLKAVDNTCKLNSL 300
DB 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLNCSPYHIVIFDLTLARLKAVDNTCKLNSL 300

QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFSPWRSSSL 360
DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFSPWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 7
ABP81789
ID ABP81789 standard; protein; 372 AA.
XX
AC ABP81789;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human CXK chemokine receptor 5 protein SEQ ID NO:60.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX

DR WPI; 2003-046718/04.
XX N-PSDB; AB242633.
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYSL 60

QY 61 IFLGVGNVLVILVILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
DB 61 IFLGVGNVLVILVILRHROTSSSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120

QY 121 LCKTVIALHKVNFYCSLLACIAVDRLAIVHAYHRRLLSIHITCGTILVGFLL 180
DB 121 LCKTVIALHKVNFYCSLLACIAVDRLAIVHAYHRRLLSIHITCGTILVGFLL 180

QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAMFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAMFTSRFLYHVAGFLLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLNCSPYHIVIFDLTLARLKAVDNTCKLNSL 300
DB 241 VVHRLQAQRPRQOKAVRVAILVTSIFFLNCSPYHIVIFDLTLARLKAVDNTCKLNSL 300

QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFSPWRSSSL 360
DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFSPWRSSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 8
ADC22585

ID ADC22585 standard; protein; 372 AA.
XX AC ADC22585;
XX DT 18-DEC-2003 (first entry)
XX DE Human G protein-coupled receptor (GPCR) polypeptide #19.
XX KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
XX KM intracellular-3 region; IC3; receptor.
XX OS Homo sapiens.
XX PN US655339-B1.
XX PD 29-APR-2003.
XX PF 13-OCT-1998; 98US-00170496.
XX PR 14-APR-1997; 97US-00839449.
XX PR 14-APR-1998; 98US-00060188.
XX PR 26-JUN-1998; 98US-0090783P.
XX PR 07-AUG-1998; 98US-0095677P.
XX PA (AREN-) ARENA PHARM INC.
XX PI Liaw CW, Behan DP, Chalmers DT;
XX DR WPI; 2003-742861/70.
XX DR N-PSDB; ADC22584.
XX PT Creating a constitutively active version of an endogenous human G protein
XX PT coupled receptor (GPCR) comprises substituting a specific amino acid in
XX PT the transmembrane-6 region with a different amino acid, and testing for
XX PT constitutive activity.
XX PS Example 1; SEQ ID NO 66; 221pp; English.
XX CC The invention relates to a method for treating a non-endogenous,
XX CC constitutively active version of an endogenous human G protein-coupled
XX CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
XX CC intracellular-3 (IC3) region, by substituting a specific amino acid in
XX CC the TM6 region with a different amino acid, and testing for constitutive
XX CC activity. The method is useful for creating a constitutively active
XX CC version of an endogenous human GPCR that comprises a transmembrane 6
XX CC region and an intracellular loop 3 region. The altered human GPCR
XX CC polypeptides are useful for screening test compounds for identification
XX CC of inverse agonists or partial agonists of GPCR polypeptides, which may
XX CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
XX CC vitro in biological research. A nucleic acid encoding the altered GPCR
XX CC may be used to create a transgenic animal expressing the altered GPCR.
XX CC The method allows screening for compounds that modulate the activity of a
XX CC human G protein-coupled receptor without the need for provision of a
XX CC ligand for the receptor. This is particularly useful in allowing
XX CC screening of compounds against orphan receptors for which no ligand is
XX CC currently known. This sequence represents a human GPCR polypeptide of the
XX CC invention.
XX SQ Sequence 372 AA;
Query Match 100.0%; Score 1953; DB 7; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPTATEGLMASFKAVFPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRLDNDYNTSLVENHLCPTATEGLMASFKAVFPVAYS 60
QY 61 IFLLGVIGNVLLVILVILVILVILVILVILVILVILVILVILVILVILVILVILVILV 120
DB 61 IFLLGVIGNVLLVILVILVILVILVILVILVILVILVILVILVILVILVILVILVILV 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVAHYRHRRLLSIHITCGTIWLVGFL 180

DB 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIHVAHYRHRRLLSIHITCGTIWLVGFL 180
QY 181 ALPEILFAKVSQGHNSLPCTFSQENQAETHAFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNSLPCTFSQENQAETHAFTSRFLYHVAGFLPMLVMGWCYVG 240
QY 241 VVHRLRQARRPQROKAVRVAILVTSIFFLCWSPHYHIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLRQARRPQROKAVRVAILVTSIFFLCWSPHYHIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSLLTKLGCTGPASLCOLPSPWRRSSL 360
DB 301 PVAITMCEFLGLAHCCINPMLYTFAGVKFRSDLSLLTKLGCTGPASLCOLPSPWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 9
ADH14058
ID ADH14058 standard; protein; 372 AA.
XX AC ADH14058;
XX DT 11-MAR-2004 (first entry)
XX DE Human BLR1.
XX KW human; non-endogenous; G protein-coupled receptor; GPCR; receptor.
XX OS Homo sapiens.
XX PN US2003105292-A1.
XX PD 05-JUN-2003.
XX PF 20-SEP-2002; 2002US-00251385.
XX PR 26-JUN-1998; 98US-0090783P.
XX PR 07-AUG-1998; 98US-0095677P.
XX PR 13-OCT-1998; 98US-00170496.
XX PA (LIAM/) LIAM C W.
XX PA (BEHA/) BEHAN D P.
XX PA (CHAL/) CHALMERS D T.
XX PI Liaw CW, Behan DP, Chalmers DT;
XX DR WPI; 2003-801247/75.
XX DR N-PSDB; ADH14057.
XX PT New constitutively active, non-endogenous version of an endogenous human
XX PT G protein-coupled receptor for the identification of therapeutic
XX PT compounds, such as agonists.
XX PS Example 1; SEQ ID NO 66; 227pp; English.
XX CC The invention relates to a constitutively active, non-endogenous version
XX CC of an endogenous human G protein-coupled receptor (GPCR). The GPCR is
XX CC used for screening therapeutic compounds as inverse agonists, agonists or
XX CC partial agonists. The GPCR can be also be used to elucidate and
XX CC understand the roles of GPCRs in normal and diseased humans. The GPCR
XX CC need not be purified and isolated to be used to screen for therapeutic
XX CC compounds. The utility of the GPCR as a research tool is enhanced because
XX CC the role of a particular receptor can be understood before the endogenous
XX CC ligand is identified. The present sequence is used in the exemplification
XX CC of the present invention.
XX SQ Sequence 372 AA;
Query Match 100.0%; Score 1953; DB 7; Length 372;

PN WO2004040000-A2.
 XX 13-MAY-2004.
 XX 09-SEP-2003; 2003WO-US028226.
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX (PRIM-) PRIMAL INC.
 XX
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F,
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
 XX
 XX WPI; 2004-390329/36.
 DR N-PSDB; ADO29818.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX
 XX Claim 151; SEQ ID NO 300; 542pp; English.
 PS
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 8; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.8e-196;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPFTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGFLMASFKAFVFPVAYSL 60
 DB 1 MNYPFTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGFLMASFKAFVFPVAYSL 60
 QY 61 IFLGVIGNVLVLILVILHRHQRTRSTETFLFLHVLADLLVFLPFAVAGSVGVWLGTG 120
 DB 61 IFLGVIGNVLVLILVILHRHQRTRSTETFLFLHVLADLLVFLPFAVAGSVGVWLGTG 120
 QY 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAIHVAVHYRHRLLSIHITCGTIWLGVFL 180
 DB 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAIHVAVHYRHRLLSIHITCGTIWLGVFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
 XX |||||
 DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
 QY 241 VVHRLQAQRORPOROKAVRAVAILVTISIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
 DB 241 VVHRLQAQRORPOROKAVRAVAILVTISIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
 QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRSSSL 360
 DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLPFSWRSSSL 360
 QY 361 SESENATSLTTP 372
 DB 361 SESENATSLTTP 372

RESULT 12
 ADR66972
 ID ADR66972 standard; protein; 372 AA.
 XX
 AC ADR66972;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human cancer associated protein sequence SEQ ID NO:18.
 XX
 KW cancer; cancer associated nucleic acid; cancer associated gene;
 KW cancer associated protein; CAP; cytostatic; vaccine; gene therapy;
 XX lymphoma; leukaemia; human.
 OS Homo sapiens.
 XX
 PN WO2004074321-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US005000.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 23-SEP-2003; 2003US-00669920.
 PR 15-DEC-2003; 2003US-00737318.
 XX (SAGR-) SAGRES DISCOVERY INC.
 PA
 XX Morris DW, Malandro MS;
 PI
 XX WPI; 2004-852915/63.
 DR N-PSDB; ADR66970, ADR66971.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS Claim 18; SEQ ID NO 18; 166pp; English.
 XX
 XX The present invention describes an isolated cancer associated (CA)
 CC nucleic acid (1). Also described: (1) an expression vector comprising (1)
 CC ; (2) a host cell comprising (1) or the expression vector; (3) a
 CC microarray for detecting a CA nucleic acid; (4) an isolated cancer
 CC associated protein (CAP) polypeptide, encoded within an open reading
 CC frame of a CA sequence; (5) an isolated antibody, or its antigen binding
 CC fragment, that binds to the above polypeptide; (6) a hybridoma that
 CC produces the above monoclonal antibody; (7) a pharmaceutical composition
 CC comprising the above antibody and a pharmaceutical excipient; (8) a kit
 CC for detecting cancer cells, comprising the (monoclonal) antibody
 CC described above; (9) methods for diagnosing cancer or for detecting the
 CC presence or absence of cancer cells in an individual; (10) a method for
 CC inhibiting growth of cancer cells in an individual; (11) a method for
 CC delivering a therapeutic agent to cancer cells in an individual; (12) an
 CC electronic library comprising the above polynucleotide or polypeptide, or

CC their fragments; (13) methods of screening for anticancer activity or for
CC a bioactive agent capable of modulating the activity of a CAP; (14)
CC methods for detecting cancer associated with expression of a polypeptide
CC in a test cell sample, or with the presence of an antibody in a test
CC serum sample; (15) a method for treating cancers; and (16) a method for
CC inhibiting the expression of CA gene in a cell. The CA sequences have
CC cytostatic activity, and can be used in vaccines, and in gene therapy.
CC The composition and methods are useful for detecting, diagnosing,
CC preventing and treating cancers, especially lymphoma and leukaemia. They
CC may also be used in screening for agents that modulate cancer. The
CC present sequence represents a cancer associated protein (CAP) sequence,
CC which is used in the exemplification of the present invention.
XX
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1953; DB 8; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGEGPLMASFKAVFPVAYSL 60
QY 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
DB 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120
QY 121 LCKTVIALHKVNFYCSLLACIADVRYLAIVHAVYHRRHLLSIHITCGTTLWVGFL 180
DB 121 LCKTVIALHKVNFYCSLLACIADVRYLAIVHAVYHRRHLLSIHITCGTTLWVGFL 180
QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAMFTSRFLYHAGFLPMLVNGCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAMFTSRFLYHAGFLPMLVNGCYVG 240
QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVFLDTLARKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVFLDTLARKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCCNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRSSSL 360
DB 301 PVAITWCEFLGLAHCCNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRSSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 13
ID ABB11873
XX ABB11873 standard; peptide; 378 AA.
AC ABB11873;
XX
DT 11-JAN-2002 (first entry)
XX Human Burkitt lymphoma receptor homologue, SEQ ID NO:2243.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer.
XX
OS Homo sapiens.

XX WO200157188-A2.
DN
XX 09-AUG-2001.
PD
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-457740/49.
DR
XX N-PSDB; ABA09117.
XX
XX Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
XX Claim 20; Page 269; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX
SQ Sequence 378 AA;

Query Match 100.0%; Score 1953; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.8e-196;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGEGPLMASFKAVFPVAYSL 60
DB 7 MNYPLTLEMDLENLEDFWELDRDLDYNDTSLVENHLCPTGEGPLMASFKAVFPVAYSL 66
QY 61 IFLLGVIGNVLVILERHROTSTRSTETFLFLAVADLLVFLPFAVAGSGVWLGTF 120

Db 67 IFLLGVGNVLVILSRHRQTRSTETFLFHLAVADLLLVFLPFAVAGSVGVVLGTF 126
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHVAYHRRLLSIHITCGTIWLVGFL 180
Db 127 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHVAYHRRLLSIHITCGTIWLVGFL 186
Qy 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLLPMLVMGWCYVG 240
Db 187 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLLPMLVMGWCYVG 246
Qy 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPHYHIVFLDTLRLKAVDNTCKLNGSL 300
Db 247 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPHYHIVFLDTLRLKAVDNTCKLNGSL 306
Qy 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
Db 307 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 366
Qy 361 SESENATSLTTF 372
Db 367 SESENATSLTTF 378

RESULT 14

AA90661
ID AAY90661 standard; protein; 372 AA.

XX AC AAY90661;

XX DT 21-AUG-2000 (first entry)

XX DE Human mutant G protein-coupled receptor BLR1 (V258K).

XX KW G protein-coupled receptor; GPCR; constitutively active;

XX KW intracellular loop 3; transmembrane domain 6; drug screening; agonist;

XX KW antagonist; mutant; mutein.

XX KW Homo sapiens.

XX QS Synthetic.

XX PN W0200022129-A1.

XX PD 20-APR-2000.

XX PF 12-OCT-1999; 99WO-US023938.

XX PR 13-OCT-1998; 98US-00170496.

XX PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Chalmers DT, Liaw CW;

XX DR WPI; 2000-329165/28.

XX DR N-PSDB; AAA30727.

XX PT Non-endogenous constitutively activated human G protein-coupled
XX PT receptors, useful for identifying agonists for use as pharmaceutical
XX PT agents.

XX PS Example 2; Page 254-256; 341pp; English.

XX CC The invention relates to constitutively active, non-endogenous versions
XX CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
XX CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
XX CC and AAA30775-A30779). The mutant proteins of the invention contain a
XX CC mutation in a portion of the protein comprising intracellular loop 3
XX CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
XX CC is substituted for an endogenous residue in IC3 at a position 16 amino
XX CC acids N-terminal of an endogenous proline in TM6 to form a sequence X-
XX CC (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
XX CC Ala, and is preferably Lys. When the endogenous residue at this position
XX CC is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
XX CC amino acid stretch between the substituted amino acid and the Pro may be

CC endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC residues. The constitutively active GPCRs are useful for identifying
CC antagonists, agonists and partial agonists for use as pharmaceutical
CC agents. The mutant proteins are also useful in research settings for
CC elucidating the roles of the receptors in normal and diseased conditions.
CC Antagonists for a particular GPCR are useful for treating diseases and
CC disorders associated with that receptor. Because the novel mutant GPCRs
CC are constitutively active, they can be used directly for screening of
CC compounds without the need for endogenous ligands. Sequences AAY90643-
CC AAY90677 and AAY90683-Y90687 the mutant human GPCRs of the invention
XX SQ Sequence 372 AA;

Query Match 99.7%; Score 1947; DB 3; Length 372;

Best Local Similarity 99.7%; Pred. No. 7.5e-196;

Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNYPTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPTATGFLMASPKAVFPVAYS 60

Db 1 MNYPTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPTATGFLMASPKAVFPVAYS 60

Qy 61 IFLLGVGNVLVILSRHRQTRSTETFLFHLAVADLLLVFLPFAVAGSVGVVLGTF 120

Db 61 IFLLGVGNVLVILSRHRQTRSTETFLFHLAVADLLLVFLPFAVAGSVGVVLGTF 120

Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHVAYHRRLLSIHITCGTIWLVGFL 180

Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAIYHVAHVAYHRRLLSIHITCGTIWLVGFL 180

Qy 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLLPMLVMGWCYVG 240

Db 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHAGFLLPMLVMGWCYVG 240

Qy 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPHYHIVFLDTLRLKAVDNTCKLNGSL 300

Db 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPHYHIVFLDTLRLKAVDNTCKLNGSL 300

Qy 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

Db 301 PVAITMCEFLGLAHCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360

Qy 361 SESENATSLTTF 372

Db 361 SESENATSLTTF 372

RESULT 15

ADC22719

ID ADC22719 standard; protein; 372 AA.

XX AC ADC22719;

XX DT 18-DEC-2003 (first entry)

XX DE Human G protein-coupled receptor (GPCR) polypeptide #58.

XX KW Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
XX KW intracellular-3 region; IC3; receptor.

XX OS Homo sapiens.

XX PN US6555339-B1.

XX PD 29-APR-2003.

XX PF 13-OCT-1998; 98US-00170496.

XX PR 14-APR-1997; 97US-00839449.

XX PR 14-APR-1998; 98US-00060188.

XX PR 26-JUN-1998; 98US-0090783P.

XX PR 07-AUG-1998; 98US-0095677P.

XX PA (AREN-) ARENA PHARM INC.

XX Liaw CW, Behan DP, Chalmers DT;
XX WPI; 2003-742861/70.
DR N-PSDB; ADC22718.
XX
PT Creating a constitutively active version of an endogenous human G protein
PT coupled receptor (GPCR) comprises substituting a specific amino acid in
PT the transmembrane-6 region with a different amino acid, and testing for
PT constitutive activity.
XX
XX Example 2; SEQ ID NO 200; 221pp; English.
PS
XX
CC The invention relates to a method for treating a non-endogenous,
CC constitutively active version of an endogenous human G protein-coupled
CC receptor (GPCR) that has a transmembrane-6 (TM6) region and an
CC intracellular-3 (IC3) region, by substituting a specific amino acid in
CC the TM6 region with a different amino acid, and testing for constitutive
CC activity. The method is useful for creating a constitutively active
CC version of an endogenous human GPCR that comprises a transmembrane 6
CC region and an intracellular loop 3 region. The altered human GPCR
CC polypeptides are useful for screening test compounds for identification
CC of inverse agonists or partial agonists of GPCR polypeptides, which may
CC have therapeutic uses. The altered GPCRs may also be used in vivo or in
CC vitro in biological research. A nucleic acid encoding the altered GPCR
CC may be used to create a transgenic animal expressing the altered GPCR.
CC The method allows screening for compounds that modulate the activity of a
CC human G protein-coupled receptor without the need for provision of a
CC ligand for the receptor. This is particularly useful in allowing
CC screening of compounds against orphan receptors for which no ligand is
CC currently known. This sequence represents a human GPCR polypeptide of the
XX invention.
XX
SQ Sequence 372 AA;

.Query Match 99.7%; Score 1947; DB 7; Length 372;
Best Local Similarity 99.7%; Pred. No. 7.Se-196;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNYPLTLENDLEDFWELDRDNDYNTSLVENHLCPCATEGLMASFKAVFVPVAYSL 60
DB 1 MNYPLTLENDLEDFWELDRDNDYNTSLVENHLCPCATEGLMASFKAVFVPVAYSL 60

QY 61 IFLLGVIGNVLVILVILRHQRQTSSTETFLFHLAVADLLVFLPFAVAEGSVGWLGTF 120
DB 61 IFLLGVIGNVLVILVILRHQRQTSSTETFLFHLAVADLLVFLPFAVAEGSVGWLGTF 120

QY 121 LCKTVIALHKVNYFCSSLLACIADRYLAIVHAVYHRRRLLSHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNYFCSSLLACIADRYLAIVHAVYHRRRLLSHITCGTIWLVGFL 180

QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQAKRVAILVTSIFFLCMSPHYHIVFDTLARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQAKRVAILVTSIFFLCMSPHYHIVFDTLARLKAVDNTCKLNGSL 300

QY 301 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360
DB 301 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLFPSWRRSSL 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:47:36 ; Search time 41 Seconds
(without alignments)
872.991 Million cell updates/sec

Title: US-10-666-689-6
 Perfect score: 1953
 Sequence: 1 MNYPITLMDIENLEDLFE.....PSWRRSSUSESENATSLTTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	1953	100.0	372	2	S25667	G protein-coupled	
2	1700	87.0	327	2	S56162	MDGR15 protein - h	
3	1635	83.7	374	2	S42628	G protein-coupled	
4	1590	81.4	374	2	S32785	G protein-coupled	
5	615	31.5	367	2	JE0349	interferon-inducib	
6	601.5	30.8	360	2	A53611	interleukin-8 rece	
7	596	30.5	378	2	B55735	lymphocyte-specifi	
8	574	29.4	378	2	A45680	G protein-coupled	
9	571.5	29.3	378	2	A55735	G protein-coupled	
10	569	29.1	355	2	QJ1231	interleukin-8 rece	
11	561	28.7	350	2	A53945	interleukin-8 rece	
12	547	28.0	358	2	A35752	interleukin-8 rece	
13	543	27.8	352	2	G00048	fusin (LESTRA) - c	
14	540	27.6	352	2	A45747	neuropeptide Y/pep	
15	537.5	27.5	353	2	S28787	neuropeptide Y/pep	
16	536	27.4	356	2	S42096	interleukin-8 rece	
17	519.5	26.6	359	2	A48921	interleukin-8 rece	
18	499.5	25.6	354	2	A23669	interleukin-8 rece	
19	497	25.4	355	2	JC5067	G protein-coupled	
20	495.5	25.4	360	2	JC5587	chemokine (C-C) re	
21	494.5	25.3	369	2	JC5068	G protein-coupled	
22	479.5	24.6	360	2	A57160	chemokine (C-C) re	
23	474	24.3	355	2	I49339	macrophage inflamm	
24	465	23.8	360	2	JC3443	chemokine (C-C) re	
25	461.5	23.6	354	2	I58186	probable G protein	
26	461.5	23.6	374	2	I38450	chemokine (C-C) re	
27	461	23.6	352	2	A43113	chemokine (C-C) re	
28	455	23.3	355	2	A45177	chemokine (C-C) re	
29	450	23.0	383	2	S55594	G protein-coupled	

ALIGNMENTS

RESULT 1

S26667

G protein-coupled receptor BLR1 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S26667

R:Dobner, T.; Wolf, I.; Enrich, T.; Lipp, M.

Eur. J. Immunol. 22, 2795-2799, 1992

A:Title: Differentiation-specific expression of a novel G protein-coupled receptor for fructose

A:Reference number: S26667; MUID:93049615; PMID:1425907

A:Accession: S26667

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-372 <DOB>

A:Cross-references: UNIPROT:P32302; EMBL:X68149; NID:G29459; PIDN:CAA48252.1; PID:G29459

C:Genetics:

A:Gene: GDB:BLR1

A:Cross-references: GDB:136235; OMIM:601613

A:Map position: 15q26.1-15q26.1

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	100.0.0%;	Score	1953;	DB	2;	Length	372;
Best Local Similarity	100.0.0%;	Pred. No.	1.7e-162;				
Matches	372;	Conservative	0;	Mismatches	0;	Indels	0;
Gapø	0;						
Qy	1	MNYPLTLEMDLENLEDLFWELDRDLNDYNDTSLVENHLCPATEGPLMASFKAFVFPVAYSL	60				
Db	1	MNYPLTLEMDLENLEDLFWELDRDLNDYNDTSLVENHLCPATEGPLMASFKAFVFPVAYSL	60				
Qy	61	IFPLGIVGNVLVILIERHRQTRSSSTETFFHLAVADLLVFLILPFAVAGSUGVWLGTFF	120				
Db	61	IFPLGIVGNVLVILIERHRQTRSSSTETFFHLAVADLLVFLILPFAVAGSUGVWLGTFF	120				
Qy	121	LCKTVIALHKVNYFCSSLLACIADVRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL	180				
Db	121	LCKTVIALHKVNYFCSSLLACIADVRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL	180				
Qy	181	ALPEILLPAKYSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGELLPMLVMGWCYVG	240				
Db	181	ALPEILLPAKYSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGELLPMLVMGWCYVG	240				
Qy	241	VHRLRQARRPORQAKRVAILVTISIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL	300				
Db	241	VHRLRQARRPORQAKRVAILVTISIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL	300				
Qy	301	PVAITWCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL	360				
Db	301	PVAITWCEFLGLAHCCINPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL	360				
Qy	361	SSENAATSLTTF	372				


```
QY 239 VGVVHRLRQRRPQOKAVRVAILVTSIFFLCWSPHYHIFLDTLRLKAVDNTCKLNG 298
Db 241 VGVVHRLRQRRPQOKAVRVAILVTSIFFLCWSPHYHIFLDTLRLKAVNSCELSG 300
QY 299 SLPVAITMCEFLGLAHCCCLNPMLYTFAGVFRSDLSRLTLKLGCTGPASICQLPFPWSRRS 358
Db 301 YLSVAITLCEFLGLAHCCCLNPMLYTFAGVFRSDLSRLTLKLGCTGPASICQLPFPWGRKS 360
QY 359 SLSESENATSLTTF 372
Db 361 SLSESENATSLTTF 374

RESULT 5
JE0349
interferon-inducible protein 10 (ip-10) receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C:Accession: JE0349
R:Tamari, M.; Tomimaga, Y.; Yatsunami, K.; Narumi, S.
Biochem. Biophys. Res. Commun. 251, 41-48, 1998
A:Title: Cloning of the murine interferon-inducible protein 10 (IP-10) receptor and its
A:Reference number: JE0349; MUID:99009219; PMID:9790904
A:Accession: JE0349
A:Molecule type: mRNA
A:Residues: 1-367 <TAM>
A:Cross-references: UNIPROT:Q9QW6; DBJ:AB003174; NID:G3798731; PIDN:BA34045.1; PID:G3798731
C:Comment: This protein is important for lymphocyte trafficking to lymphoid organs.
C:Superfamily: vertebrate rhodopsin

Query Match 31.5%; Score 615; DB 2; Length 367;
Best Local Similarity 38.8%; Pred. No. 5.7e-46;
Matches 134; Conservative 59; Mismatches 139; Indels 14; Gaps 6;

QY 28 NDTSLVENHLCPCATEGPMASFKAVFPVAVYSILFLLGVGNVVLVILRHRHQTSSSTE 87
Db 32 NESDFSDSPCPQ---DFSLNFORTFLPALYSLLFLGLGNGAVAAVLLSQRTALSSTD 88
QY 88 TFLFLAVADLLAVFLPFPAAVSGSVGVLGTFLLCKTIVLHKVNFVCSLLIACIAVD 147
Db 89 TFLFLAVADLLAVFLPFPAAVSGSVGVLGTFLLCKTIVLHKVNFVCSLLIACIAVD 148
QY 148 YLAIVHAVHAYRHRLLSIHITCGTIWLGFLFLALPEILFAKVSQGHNNSLPRCTFSOE 207
Db 149 YLSIVHATQYRDRPRVVALTCIVVWGLCLLFPDFIYLSANYQRLNA-THCQYNFP 207
QY 208 NQAEHAWFTSRFLYHVGFLPMLVWGCYGVVHRLRQARRPQOKAVRVAILVTSI 267
Db 208 QVGRG---ALRVQLVAGFLPLLVMAVYAHILAVL-LVSRGQRFRAMRLVVVVVAA 262
QY 268 FFLCWSPHYHIFLDTLRLKAVDNTCKLNGSLPVAITMCEFLGLAHCCCLNPMLYTFAGV 327
Db 263 FAVCWTPYHLVLDVLDMDVGLARNCGRESHVDVAKSVTSGMGYHCCCLNPLLYAFVG 322
QY 328 KFRDLSRLTLKLGCT---GPASICQLPFPWSRRSSLSSENATSL 369
Db 323 KFREQMMLFTRIGRSDQGRQ---QPSSSRRESSWSSETTEASYL 365

RESULT 6
A53611
interleukin-8 receptor type B - human
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C:Accession: I37898; I378712; A53611; A39446
R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A:Title: Comparison of the genomic organization and promoter function for human interleukin-8
A:Reference number: I37898; MUID:95014476; PMID:7929358
A:Accession: I37898
A>Status: preliminary
A:Molecule type: DNA
```

```
A:Residues: 1-360 <RES>
A:Cross-references: UNIPROT:P25025; EMBL:U11869; NID:G511801; PIDN:AA860656.1; PID:G511869;
A:Accession: I378712
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <RE2>
A:Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA64380.1; PID:G511809; EMBL:U11872;
I1876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878;
R:Spranger, H.; Lloyd, A.R.; Lautens, L.L.; Bonner, T.I.; Kelvin, D.J.
J. Biol. Chem. 269, 11065-11072, 1994
A:Title: Structure, genomic organization, and expression of the human interleukin-8 r
A:Reference number: A53611; MUID:94209273; PMID:7512557
A:Accession: A53611
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 6-360 <SPR>
A:Cross-references: GB:M99412; GB:L19593
R:Murphy, P.M.; Tiffany, H.L.
Science 253, 1280-1283, 1991
A:Title: Cloning of complementary DNA encoding a functional human interleukin-8 recept
A:Reference number: A39446; MUID:91368200; PMID:1891716
A:Accession: A39446
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 6-360 <MUR>
A:Cross-references: GB:M73969
C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8,
C:Genetics:
A:Gene: GDB:IL8RB; IL8RA
A:Cross-references: GDB:127868; OMIM:146928
A:Map position: 2q35-2q35
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 30.8%; Score 601.5; DB 2; Length 360;
Best Local Similarity 38.6%; Pred. No. 8.4e-45;
Matches 141; Conservative 57; Mismatches 154; Indels 13; Gaps 8;

QY 9 MDLENLEDFWELDRDLDNYNDTSLVENHLCPCATE-GPLMASFKAVFPVAVYSILFLLGVI 67
Db 6 MESDSFED-FWKGEDLSNYSYSTLPFLDDAAPCEPESELEINKYFVVIYALVFLSL 64
QY 68 GNVVLVILRHRHQTSSSTETFLHVLADLLLVILPFPAAVSGSVGVLGTFLLCKTVIA 127
Db 65 GNSLVMLVILYSRGVSVDVYLLNLADLLFALTLPVAAASKVNGWIFGTFLLCKVSL 124
QY 128 LHKVNFYCSLLIACIAVDRLVAVHAYRHRLLSIHITCGTIWLGFLFLALPEILP 167
Db 125 LKEVNFYSGILLIACISVDRLVAVHATRTLTOKRYL-VKFCISLWGLSLLALPVL 163
QY 168 AKVSGQHNNSLPRCTFSQENQAEHAW-FTSRFLYHVGFLPMLVWGCYGVVHRLR 246
Db 164 RRTV--YSNVSPACVEDMGN--NTANRMLLRILPQSGFIVPLLIIMLFCYGTTLTLF 239
QY 247 QAQRPPQOKAVRVAILVTSIFFLCWSPHYHIFLDTLRLKAVDNTCKLNGSLPVAITM 306
Db 240 KA-HMGQKRAMRVFAVVLIFLLCWLPLYNLADLLTMRQTQVIOETCERRRHIDRALDA 298
QY 307 CEFGLAHCCCLNPMLYTFAGVFRSDLSRLTLKLGCTGPASICQLPFPWSRRSSLSSENA 366
Db 299 TEILGILHSCCLNPLIYAFIQGRHGLKILAIHGLSKDSL----PKDSRPSFVGSSG 354
QY 367 TSLTT 371
Db 355 HTSTT 359

RESULT 7
B55735
lymphocyte-specific G protein-coupled receptor EB11 - human
N:Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein 1
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
```

C;Keywords: G protein-coupled receptor; transmembrane protein	
Query Match	29.4%; Score 574; DB 2; Length 378;
Best Local Similarity	35.9%; Pred. No. 2.2e-42;
Matches	126; Conservative 78; Mismatches 125; Indels 22; Gaps 9
Qy	29 DTSLVENHILCPATEGPLMASFKAFVPAVASYLIPELLGVIGNVILVILVILRHROTSSSTET 88
Db	40 DYTLFES-LCSKCD--VRNPFKAWFLPIMYSIICFVGLLGNGLVLTYYFKRLKTKMTDT 95
Qy	89 FLFLHVLADLLLVFLPFAVAGSGVWGLTFLCKTIALHKKVNFYCSLLIACIACVDRY 148
Db	96 YLLNLAVADILFLTLFPWYSAKSVFVGFHFKLIPAIYKMSFFSGWLLLCISIDRY 155
Qy	149 LAIVHAVHYRHR--LLSIHITCGTITWLVGFLALPEILPAKVSQGHNNNSLPCTFSQ 206
Db	156 VAIVQAVSAHRHRARVLLISKLCVGSAILATVLSIPELLYSDIQRSSSEQAM-RCSLIT 214
Qy	207 ENQAETHAWTSRFLYHVAGFLDPMLVNMGCVGVVHRLRQAQRPPQOKAVRVAILVTS 266
Db	215 EH---VEAFITIOVQWVIGFLVPLLAMSFCLYLIIRTLLQA-RNFERNKAIVKIVAVV 270
Qy	267 IFLCWSPIHYIVFLDTLARIKAVDNTCKLNGSLPVAITWCETFLGLAHCCLNPMLYTPAG 326
Db	271 VFTVFOQPYNGVLAQTVANFIITSSCELSKQNIAYDVITYSLACVRCVWPNFLYATIG 330

```

Qy   327 VKFRSDLSRLTLTKLGCTGPASLCOLFPSW-----RBSLS-ESENATSLT 370
      |||||:::|||       |||||::||::|:|:|:|
Db   331 VKPRNDFIKFLKDLGCLGSQBQLRQ---WSSCRHRRSSVSEAEITTFIS 377

RESULT 9
A55735
G protein-coupled receptor EBII - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C/Accession: A55735
R/Schweickart V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; S.L.; S.
Genomics 23, 643-650, 1994
A>Title: Cloning of human and mouse EBII, a lymphoid-specific G-protein-coupled
A/Reference number: A55735; MUID:95154835; PMID:7851893
A/Accession: A55735
A>Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-378 <SCH>
A/Cross-references: UNIPROT:P47774; GB:L31580; NID:G468340; PIDN:AAA74232.1; P
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor

Query Match          29.3%; Score 571.5; DB 2; Length 378;
Best Local Similarity 36.7%; Pred. No. 3.6e-42;
Matches 120; Conservative 71; Mismatches 129; Indels 7; Gaps 4
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55 NFRAWFLPLMYSVICFVGLLGNGLVILTYVFKRLKMTDITYLLNLAVADYLFLLILPFW 111
108 VAGSVGVWLTGELCKTVIALHKHKNFYCSSILLACIADVRLYALVHVAHYHRHR - LLS 165
115 AYEBAKSWIFGVYDCKGIFGYIKLUSFFSGMLLLCISIDRVVAIVQVSRHRHRAVLLI 174
166 IHITCGTIVLWGLLALPEILFAKVSGQHNNNSLPRCTFSSQENQAETHAWTSTRFLYHVA 225
175 SKLSCVGIWMLALFSLIPELLYSLQNSGEDTL-RCSLV---SAQVESALITIQVAQWVF 230
226 GFLLPMLVMGVCYGVVHRLRQARRQOROKAVRAVILVTSIFFLCWSFYHIVIPDLTLA 285
231 GFLVPLMAMSFYLLIIRTLLQA-RNEFRNKAIKVIAVVVVVIFVQLPYNGVVLAAQTVA 289
286 RLKAVDNTCKLNGSLPVAITMCEPFLGLAHCLNPMLYTFAGVKPRSDLSRLLTKLGCCTGP 345
290 NFMITNSSCSTSKQLNAYDVTYLSASVRCCVNFPLVAFYGVKFRSDDLFKLKKOLGCLSQ 349

Qy 346 ASLCQLPFWRRSSLSSENATSLTTF 372
Db 350 ERLRHWSRCRHVRNASVMEATTTTF 376

RESULT 10

QJ1231
interleukin-8 receptor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
A/Accession: JQ1231; A46483
R/Beckmann, M.P.; Mungler, W.E.; Kozlosky, C.; VandenBos, T.; Price, V.; Lyman, S.; Gerard, J.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Biochem. Biophys. Res. Commun. 179, 784-789, 1991
A/Title: Molecular characterization of the interleukin-8 receptor.
A/Reference number: JQ1231; MUID:91378994; PMID:1898400
A/Accession: JQ1231
A/Molecule type: DNA
A/Residues: 1-355 <BEC>
A/Cross-references: UNIPROT:P21109; GB:M74240; NID:G165439; PIDN:AAA31375.1; PID:G165439
R/Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
J. Immunol. 148, 1261-1264, 1992
A/Title: Characterization of complementary DNA clones encoding the rabbit IL-8 receptor.
A/Reference number: A46483; MUID:92148149; PMID:1737938
A/Accession: A46483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-355 <LEE>
A/Cross-references: GB:M82873; NID:G165440; PIDN:AAA31376.1; PID:G165441
A/Experimental source: neutrophils
A/Note: sequence extracted from NCBI backbone (NCBI:81526, NCBIP:81530)
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 29.1%; Score 569; DB 2; Length 355;
Best Local Similarity 38.3%; Pred. No. 5.6e-42; Indels 10; Gaps 7;
Matches 129; Conservative 52; Mismatches 146;

Qy 7 LEMDLENLEDF-WELDRLDNYNDTSLVENHLCPTATGSLMASFKAVFVPVAYSLIFLLG 65
Db 1 MEYVNMNTDLTWFEDEFANATGMPPEKDYSPCL--VTQTINKVYVVVIVAYLVFLS 58
Qy 66 VIGNVLVLLEHRRQTRSTETFLPHLAVADLLLVLPILFPAVAGSVGVLGTFLCKTV 125
Db 59 LLGNSLVMLVILYSRNSRSTVDVYLLNLMADLLFALTMTPIWASKEKGWIFGTPLCKV 118
Qy 126 IALHKVNFYCSLLACIADRYLAIVHAVHAYHRRLLSIHITCGTIWLVGFLALPEI 195
Db 119 SLVKEVNFYSGILLACISVDRLAIVHATRTLTQKRHL-VKFCVLCGKGLSMNLSLPP 177
Qy 186 LFAKVSQGHNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLPMLVMGVCYGVVHR 244
Db 178 LFRQVFS--PNNSPVC--YEDLGHTAKRMVLRILPHTFGLPILPLVLMFCYGTLTR 233
Qy 245 LRQAQRROPQKAVRVAILVTSIFFLCWSPYHIVFDLTARLKAVENTCKLNGSLPVAI 304
Db 234 LFQA-HMGQKRAMRVIFAVVFLLCWLPYNLVLLADTLMTHTVQETCORRNDIDRAL 292
Qy 305 TMCFEFLGLAHCLNPMLYTPAGVKFRSDLSRLTLKLG 341
Db 293 DATEILGFLHSLNPIIYAFIGNFRNGFLKMLAARG 329

RESULT 11

A39445
interleukin-8 receptor type A - human
N/Alternate names: interleukin-8 receptor, high-affinity
C/Species: Homo sapiens (man)
C/Date: 22-Jan-1993 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
A/Accession: I37449; I38710; I38711; A39445
R/Mollereau, C.; Muescattelli, F.; Mattei, M.G.; Vassart, G.; Parmentier, M.
Genomics 16, 248-251, 1993
A/Title: The high-affinity interleukin 8 receptor gene (IL8RA) maps to the 2q33-q36 region
A/Reference number: I37449; MUID:93252387; PMID:8486366

A/Accession: I37449
A/Molecule type: DNA
A/Residues: 1-350 <RES>
A/Cross-references: UNIPROT:P25024; EMBL:X65858; NID:G312046; PIDN:CAA46688.1; PID:G312046
R/Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.
J. Biol. Chem. 269, 26381-26389, 1994
A/Title: Comparison of the genomic organization and promoter function for human interleukin-8.
A/Reference number: I37898; MUID:95014476; PMID:7929358
A/Accession: I38710
A/Molecule type: DNA
A/Residues: 1-350 <RE2>
A/Cross-references: EMBL:U11870; NID:G511804; PIDN:AAA64378.1; PID:G511805
A/Accession: I38711
A/Molecule type: mRNA
A/Residues: 1-16 <RE3>
A/Cross-references: EMBL:U11871; NID:G511806; PIDN:AAA64379.1; PID:G733002
R/Holmes, W.E.; Lee, J.; Kuang, W.J.; Rice, G.C.; Wood, W.I.
Science 253, 1278-1280, 1991
A/Title: Structure and functional expression of a human interleukin-8 receptor.
A/Reference number: A39445; MUID:91368199; PMID:1840701
A/Accession: A39445
A/Molecule type: mRNA
A/Residues: 1-275, 'T', 277-350 <HOL>
A/Cross-references: GB:M68932; NID:G186369; PIDN:AAA59159.1; PID:G186370
C/Genetics:

A/Gene: GDB:IL8RA
A/Cross-references: GDB:135039; OMIM:146929
A/Map position: 2q35-2q35

C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 28.7%; Score 561; DB 2; Length 350;
Best Local Similarity 37.7%; Pred. No. 2.8e-41; Indels 22; Gaps 11;
Matches 137; Conservative 55; Mismatches 149;

Qy 11 LEMLED-LFWELDRLDNYNDTSLVENHLCPTATGSLMASFKAV---FVPVAYSLIFLL 64
Db 1 MSNITDPQWDFDL---NFTGMP-----PADEDYSPCMLETETLKNKYVVIAYALVFL 52
Qy 65 GVIGNVLVLLEHRRQTRSTETFLHVLAVADLLLVLPILFPAVAGSVGVLGTFLCKT 124
Db 53 SLGNSLVMLVILYSRNSRSTVDVYLLNLMADLLFALTMTPIWASKEKGWIFGTFLCKV 112
Qy 125 VIALHKVNFYCSLLACIADRYLAIVHAVHAYHRRLLSIHITCGTIWLVGFLALPE 184
Db 113 VSLLEKVNPFYSGILLACISVDRLAIVHATRTLTQKRHL-VKFCVLCGKGLSMNLSLPP 171
Qy 185 ILFAKVSQGHNSLPRCTFSQENQAETHAW-FTSRFLYHVAGFLPMLVMGVCYGVVH 243
Db 172 LFRQAY--HPNNSPVCYEVILGN--DTAKRMVLRILPHTFGLVPLFVLMFCYGTTLR 227
Qy 244 LRQAQRROPQKAVRVAILVTSIFFLCWSPYHIVFDLTARLKAVENTCKLNGSLPVA 303
Db 228 TLFFKA-HMGQKRAMRVIFAVVFLLCWLPYNLVLLADTLMTHTVQIESCERNINIGRA 286
Qy 304 ITMCEFLGLAHCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCO-LFPPSWRRSLSE 362
Db 287 LDATILGFLHSLNPIIYAFIGNFRNGFLKMLAHMGLVSKFEFLARHRTVSYTSSSVV 346
Qy 363 SEN 365
Db 347 SSN 349

RESULT 12

A53752
interleukin-8 receptor (clone 5B1a) - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A/Accession: A53752
R/Prado, G.N.; Thomas, K.M.; Suzuki, H.; LaRosa, G.J.; Wilkinson, N.; Folco, E.; Naval J. Biol. Chem. 269, 12391-12394, 1994
A/Title: Molecular characterization of a novel rabbit interleukin-8 receptor isotype.

A;Reference number: A53752; MUID:94230294; PMID:8175642

A;Accession: A53752

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-358 <PRA>

A;Cross-references: UNIPROT:P35344; GB:L24445; NID:9437661; PIDN:AAA13378.1; PID:9437662

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.0%; Score 547; DB 2; Length 358;

Best Local Similarity 37.2%; Pred. No. 4.7e-40;

Matches 137; Conservative 50; Mismatches 163; Indels 18; Gaps 9;

Qy 8 EMDLEN--LEDLFWELDRLDNYND--TSLVENHLCPCATGCPMLMASFKAVPVPVAYSILFL 63

Db 3 EFTWENYSYEDFFGDFSNYSYSTDLPTLLDSAPCRSES---LETNSYVVLYTYILVFL 58

Qy 64 LGVIGNVLVLILHRHQTSSTTFFLHLAVADLLVFLPFAVAGSGVGVLTGFLCK 123

Db LSLGNSLMLVILYSRSTCVTDVYLLNLAIDALLFATLPIWAASKVHGWTGFTPLCK 118

Qy 124 TVTALHKVNFYCSSLLACIADRYLAIHVAVHAYRHRLLSIHTCGTTLVGVFLIALP 183

Db VVSLVKEVNFYSGILLACISVDRLAIVHATRTMIQRHL-VKFICLSMGWGSLILSLP 177

Qy 184 EILFAKVSQGHNNSLPRCTFPOENQAETHAW-FTSRFLYHVAGFLPLMLVMGVCYGVV 242

Db ILILFRNAI--PPPNSSPVCVEDMGN--STAKRMVLAIRLQQTGFLPLVLMFLFCYVFTL 233

Qy 243 HRLRQARRRQKQAVRAILVTSIFFLCWSPHYIVFLDTLARKLAVDNTCKLSGLPV 302

Db RTLFLQA-HMGQKRAMRVIFAVVLIFLLCPLYNVLITDTLMRTHVIOETCERRNDIDR 292

Qy 303 AITWCEFLGHAHCLNPMLYTFACGKFRSDLSRLITKLGCTGPASLCQLFPSPWRRSLSE 362

Db ALDTEILGLFHSCLNPIITAFIQGKPRYGLLKILAAHGLISKEFLAK---ESRSPFVAS 349

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

A;Reference number: A53752; MUID:94230294; PMID:8175642

A;Accession: A53752

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-358 <PRA>

A;Cross-references: UNIPROT:P35344; GB:L24445; NID:9437661; PIDN:AAA13378.1; PID:9437662

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.0%; Score 547; DB 2; Length 358;

Best Local Similarity 37.2%; Pred. No. 4.7e-40;

Matches 137; Conservative 50; Mismatches 163; Indels 18; Gaps 9;

Qy 8 EMDLEN--LEDLFWELDRLDNYND--TSLVENHLCPCATGCPMLMASFKAVPVPVAYSILFL 63

Db 3 EFTWENYSYEDFFGDFSNYSYSTDLPTLLDSAPCRSES---LETNSYVVLYTYILVFL 58

Qy 64 LGVIGNVLVLILHRHQTSSTTFFLHLAVADLLVFLPFAVAGSGVGVLTGFLCK 123

Db LSLGNSLMLVILYSRSTCVTDVYLLNLAIDALLFATLPIWAASKVHGWTGFTPLCK 118

Qy 124 TVTALHKVNFYCSSLLACIADRYLAIHVAVHAYRHRLLSIHTCGTTLVGVFLIALP 183

Db VVSLVKEVNFYSGILLACISVDRLAIVHATRTMIQRHL-VKFICLSMGWGSLILSLP 177

Qy 184 EILFAKVSQGHNNSLPRCTFPOENQAETHAW-FTSRFLYHVAGFLPLMLVMGVCYGVV 242

Db ILILFRNAI--PPPNSSPVCVEDMGN--STAKRMVLAIRLQQTGFLPLVLMFLFCYVFTL 233

Qy 243 HRLRQARRRQKQAVRAILVTSIFFLCWSPHYIVFLDTLARKLAVDNTCKLSGLPV 302

Db RTLFLQA-HMGQKRAMRVIFAVVLIFLLCPLYNVLITDTLMRTHVIOETCERRNDIDR 292

Qy 303 AITWCEFLGHAHCLNPMLYTFACGKFRSDLSRLITKLGCTGPASLCQLFPSPWRRSLSE 362

Db ALDTEILGLFHSCLNPIITAFIQGKPRYGLLKILAAHGLISKEFLAK---ESRSPFVAS 349

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

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Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 363 SENATSLT 370

Db 350 SSGNTSTT 357

Qy 219 RELYHVAGFLPLMLVMGVCYGVVHRLRQARRPQKAVRAVAILVTSIFFLCWSPHYV 278

Db 200 QFQHMVGLILPGVILSCVCIISKLSHSGH-QKRKALKTTVILILAFACWLPYYIG 258

Qy 279 IFDLTLARLKAVDNTCKLSLPLVATMCEFLGHAHCLNPMLYTFAGVKFRSDLSRLLT 338

Db 259 ISIDSFILLEIIRKQCEFTVHKWISITTEALGFHCHCLNPILYALFGAKFKTSAQHALT 318

Qy 339 KLGCTGPASLCQLFPSPWRRSSLS-ESENA 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSS 348

Qy 339 KLGCTGPASLCQLFPSPWRRSSLS-ESENA 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSS 348

Qy 339 KLGCTGPASLCQLFPSPWRRSSLS-ESENA 367

Db 319 SVSRGSSLLKLSKGRGGHSSVSTESSS 348

RESULT 14

A45747

neuropeptide Y/peptide YY receptor Y3 - human

N;Alternate names: fusin; HM89; leukocyte-derived seven-transmembrane receptor LBSTR;

C;Species: Homo sapiens (man)

C;Date: 03-May-1994 #sequence revision 03-May-1994 #text change 09-Jul-2004

C;Accession: A45747; A53103; I53006; I59444; I69203; S32761

R;Fedeerspiel, B.; Melhado, I.G.; Duncan, A.M.V.; Delaney, A.; Schappert, K.; Clark-Lu

Genomics 16, 707-712, 1993

A;Title: Molecular cloning of the cDNA and chromosomal localization of the gene for a

A;Reference number: A45747; MUID:93315164; PMID:8325644

A;Accession: A45747

A;Molecule type: mRNA

A;Residues: 1-352 <P>

A;Cross-references: UNIPROT:P61073; GB:M99293; NID:9292516; PIDN:AAA16617.1; PID:9292;

R;Joelcher, M.; Geisler, T.; O'Reilly, T.; Zwahlen, R.; Baggiolini, M.; Moser, B.

J. Biol. Chem. 269, 232-237, 1994

A;Title: Cloning of a human seven-transmembrane domain receptor, LBSTR, that is highl;

A;Reference number: A53103; MUID:94103215; PMID:8276799

A;Accession: A53103

A;Molecule type: mRNA

A;Residues: 1-352 <LOE>

A;Cross-references: EMBL:X71635; NID:9297099; PIDN:CAA50641.1; PID:9297100

R;Herzog, H.; Hort, Y.J.; Shine, J.; Seibler, L.A.

DNA Cell Biol. 12, 465-471, 1993

A;Title: Molecular cloning, characterization, and localization of the human homolog t;

A;Reference number: I53006; MUID:93319629; PMID:8329116

A;Accession: I53006

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-352 <HER>

A;Cross-references: GB:L06797; NID:9414929; PIDN:AAA03209.1; PID:9414928

R;Jazin, E.E.; Yoo, H.; Blomqvist, A.G.; Yee, F.; Weng, G.; Walker, M.W.; Salton, J.; I

Regul. Pept. 47, 247-258, 1993

A;Title: A proposed bovine neuropeptide Y (NPY) receptor cDNA clone, or its human hom

A;Reference number: I59444; MUID:94052833; PMID:8234909

A;Accession: I59444

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-352 <R2>

A;Cross-references: GB:L01639; NID:9189313; PIDN:AAA16594.1; PID:9189314

R;Murata, H.; Nielsen, B.W.; Matsushima, K.

Int. Immunol. 5, 1239-1249, 1993

A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte cl

A;Reference number: I54751; MUID:94092629; PMID:7505609

A;Accession: I54751

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-352 <RES>

A;Cross-references: GB:D10924; NID:9219868; PIDN:BAA01722.1; PID:9219869

C;Genetics: GDB:NPY3R; NPY3

A;Cross-references: GDB:230002; OMIM:162643

A;Map position: 2q21-2q21

C;Superfamily: vertebrate rhodopsin

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 540; DB 2; Length 352;

Best Local Similarity 33.9%; Pred. No. 1.9e-39;

Matches	112;	Conservative	70;	Mismatches	124;	Indels	24;	Gaps	4;
Qy	47	ASFKAVFVPAVS	IFLGLVGNVLVLVILERHROTSSTETFLFLAVADLLLVFLPF	106					
Db	34	ANFNKIFLPTYS	IFLTLGIVGNGLVILVMGYQKRLSMTDKYRLHLSVADLLFVITLPF	93					
Qy	107	AVAGSGVGLTFL	CKVTIALHKNFVCSLLLACIADRYLAIVHAYHRRLLSI	166					
Db	94	WAVDAVANWTF	GNFLCKAVHYIYVNLVSSYLLILAFISLDLYLAIVHATNSORPKLLAE	153					
Qy	167	HITCGTIWLVG	FLALPEILFAKVSQ-----HNNSLPRCTFSQENQAETHAWFTS	218					
Db	154	KVVVGVWIP	ALLTIPDFIFANVSEADDRVICDRFYNDLWVVVF-----	199					
Qy	219	RELYHAGFLLP	MLVMGCVYGVVHRLRQARRQOKAVRVAILVTSIFFLCWSPHYV	278					
Db	200	QFQHMVGLTLP	GVILSCYCIITSKLSKSHGK-OKRKALKTTVILLAFACWLPYYIG	258					
Qy	279	IFDLTLARLKA	VNDTKLNGSLPVAITMCEFLGLAHGCLNPMLYTFAGVKFRSDLSRLT	338					
Db	259	ISIDSFLLERI	KQGSFENTVHKWISITBALAFFHCCLNPILYAFLGAKFKTSAQHALT	318					
Qy	339	KLGCTGPASLC	QLPSPSWRRSSLS-ESENAT	367					
Db	319	SVSRGSSLKIL	SKGKRGHSSVSTESSESS	348					
RESULT 15									
S28787									
neuropeptide Y/peptide YY receptor Y3 - bovine									
C;Species: Bos primigenius taurus (cattle)									
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004									
C;Accession: S28787									
R;Rimland, J.; Xin, W.; Sweetnam, P.; Saijoh, K.; Nestler, E.J.; Duman, R.S.									
Mol. Pharmacol. 40, 869-875, 1991									
A;Title: Sequence and expression of a neuropeptide Y receptor cDNA.									
A;Reference number: S28787; MUID:92100053; PMID:1661837									
A;Molecule type: mRNA									
A;Residues: 1-353 <RIM>									
A;Cross-references: UNIPROT:P25930; EMBL:M86739									
C;Superfamily: vertebrate rhodopsin									
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein									
Query Match 27.5%; Score 537.5; DB 2; Length 353;									
Best Local Similarity 33.6%; Pred. No. 3.1e-39;									
Matches	118;	Conservative	69;	Mismatches	145;	Indels	19;	Gaps	6;
Qy	25	DNYNDTSLVENH	L-----CPATEGPLMASFKAVFPVAVSLIFLGLVGNVLVLVILER	78					
Db	10	DNYTEDDLGSG	DYDSMKPCFREEN---AHFNRIFLPTVYSIIFLTGIVGNGLVILVMGY	66					
Qy	79	HRQTRSTETFL	HLAVADLLVFLPFAVAEGSVGWLGTFLCKTVIALHKNFYCCSL	138					
Db	67	QKRLSMTDKYR	LHLSVADLLVFLTFWAVDAVANWYFCKFLCKAVHYIYVNLVSSVL	126					
Qy	139	LLACIADRYLA	IVHAYHRRLLSIHITCGTIWLVGFLALPEILFAKVSQGHNNNS	198					
Db	127	ILAFISLDRYL	AIIVHATNSQPKLLAEKVYVGVWLPVALLTIPDLIFADIKEVDERYI	186					
Qy	199	LPRCTFSQENQ	AETHAWF-TSRFLYHVAGFLLPMLVNGCYGVGVHRLRQARRPOROKA	257					
Db	187	CDRFYPSD----	LWLVVVFQHIWVGLLPGIIVILSCYCIISKLSHS-KGYQKRKA	238					
Qy	258	VRVAILVTSIF	FLCWSPHYVIFDLTLARLKAVDNTCKLNGSLPVAITMCEFLGLAHCCCL	317					
Db	239	LKTTVILILIT	FFACWLPYYIGISIDSFILLEIIQQCEFEFSTVHKWISITBALAFFHCCL	298					
Qy	318	NPMLYTFAGVK	FRSDLSRLTLKCTGPASLCQLPSPSWRRSSLS-ESENAT	367					
Db	299	NPILYAFLGAK	FKTSAQHALTSVSRGSSLKILSKGKRGHSSVSTESSESS	349					

Search completed: August 29, 2005, 23:57:44
Job time : 42 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:46:51 ; Search time 173 Seconds
(without alignments)
1101.118 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPLFLEMDLENDLEDFWE.....PSWRSSLSSESNATSLTTF 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1953	100.0	372	1 CCR5 HUMAN	P2302 homo sapien
2	1638	83.9	374	2 Q6P3C2	Q6P3c2 mus musculus
3	1635	83.7	374	1 CCR5 MOUSE	Q04683 mus musculus
4	1590	81.4	374	1 CCR5 RAT	P34997 rattus norv
5	866.5	44.4	392	2 Q93281	Q93281 gallus gall
6	646	33.1	366	2 Q867B2	Q867b2 capra hircu
7	638.5	32.7	390	2 Q6GNE2	Q6gne2 xenopus lae
8	635	32.5	368	1 CCR3 HUMAN	P49682 homo sapien
9	635	32.5	415	2 Q72710	Q72710 homo sapien
10	615	31.5	367	2 Q9QW6	Q9qwn6 mus musculus
11	614	31.4	367	1 CCR3 MOUSE	Q8410 mus musculus
12	613	31.4	367	2 Q9J1I9	Q9j1i9 rattus norv
13	607	31.1	374	2 Q802H1	Q802h1 petromyzon
14	606	31.0	355	2 Q8H2N4	Q8h2n4 cercopithec
15	601.5	30.8	355	2 Q8H2N8	Q8h2n8 pan troglod
16	601.5	30.8	360	1 IL8B HUMAN	P25025 homo sapien
17	599.5	30.7	355	2 Q8H2N5	Q8h2n5 macaca mula
18	596.5	30.5	355	2 Q8H2N7	Q8h2n7 gorilla gor
19	596	30.5	378	1 CKR7 HUMAN	P32248 homo sapien
20	594.5	30.5	378	2 Q8H2R6	Q8h2r6 macaca mula
21	594.5	30.4	353	1 IL8B PANTR	Q28807 pan troglod
22	590.5	30.2	355	2 Q8H2N3	Q8h2n3 papio hamad
23	585.5	30.0	353	1 IL8B GORGO	Q28422 gorilla gor
24	579.5	29.7	353	1 IL8B MACMU	Q28519 macaca mula
25	577.5	29.6	352	2 Q810T4	Q810t4 cavia porce
26	576.5	29.5	378	2 Q8CAS2	Q8cas2 mus musculus
27	576	29.5	380	2 Q861S1	Q861s1 sus scrofa
28	575	29.4	378	2 Q6U2D6	Q6u2d6 rattus norv
29	571.5	29.3	378	1 CKR7 MOUSE	P47774 mus musculus
30	569	29.1	355	1 IL8A RABIT	P21109 corytolagus
31	568.5	29.1	355	2 Q8H2N6	Q8h2n6 pongo pygma

RESULT 1

ID	CCR5 HUMAN	STANDARD;	PRT;	372 AA.
AC	P12302; Q14811;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma receptor 1) (Monocyte-derived receptor 15) (MDR15).			
GN	Name=BLR1; Synonyms=CCR5;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1] _SEQUENCE FROM N.A. (ISOFORM LONG).			
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RC	TISSUE=Lymphocytes; PubMed=1425907;			
RX	MEDLINE=93049615; PubMed=1425907;			
RA	Dobner T., Wolf I., Emrich T., Lipp M.;			
RT	"Differentiation-specific expression of a novel G protein-coupled receptor from Burkitt's lymphoma.";			
RT	receptor from Burkitt's lymphoma.";			
RL	Eur. J. Immunol. 22:2795-2799(1992).			
RN	[2] _SEQUENCE FROM N.A. (ISOFORM SHORT).			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	TISSUE=Blood;			
RX	MEDLINE=95366951; PubMed=7639692;			
RA	Barella L., Loetscher M., Tobler A., Baggiolini M., Moser B.;			
RT	"Sequence variation of a novel heptahelical leucocyte receptor through alternative transcript formation.";			
RL	Biochem. J. 309:773-779(1995).			
RN	[3] _LIGAND BINDING.			
RP	MEDLINE=98130629; PubMed=9463416;			
RA	Legler D.F., Loetscher M., Stuber Roos R., Clark-Lewis I.,			
RA	Baggiolini M., Moser B.;			
RT	"B cell-attracting chemokine 1, a human CXC chemokine expressed in lymphoid tissues, selectively attracts B lymphocytes via BLR1/CXCR5.";			
RL	J. Exp. Med. 187:655-660(1998).			
CC	- FUNCTION: Cytokine receptor that binds to BLC. BLR1 exerts possibly a regulatory function in burkitt lymphoma (BL) lymphomagenesis and/or B-cell differentiation. It is a potential candidate for cell-cell interaction, and activation of mature B-lymphocytes in lymphatic tissues.			
CC	- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=2;			
CC	Name=Long;			
CC	Isoid=P32302-1; Sequence=Displayed;			
CC	Name=Short;			
CC	Isoid=P32302-2; Sequence=VSP 001892;			
CC	- TISSUE SPECIFICITY: Expression in mature B-cells and Burkitt lymphoma cells.			
CC	- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			

QY 1 MNYPLTLEMD--LENLEDFWELDRDLNNDYNTSLVENHLCPCATGELMASFKAVFVPVAY 58
 Db 1 MNYPLTLDGMSITYNDDLYKELAFYSNSTEIFLQDSNFCSTVEGELLTSFKAVFVPVAY 60
 QY 59 SLIFLLGVGNVLVLILERHRTSRSTETFLFHLAVADLLVFLPFAVAESGVGWLG 118
 Db 61 SLIFLLGMGNILVLILERHRTSRSTETFLFHLAVADLLVFLPFAVAESGVGWLG 120
 QY 119 TFLCKTVIALKHVNFYCSSLLACIADVRYLAIVHAVYHRRLLSIHTCTIWLGVF 178
 Db 121 TFLCKTVIALKHNFYCSSLLACIADVRYLAIVHAVYHRRLLSIHTCTIWLGVF 180
 QY 179 LLALPEILPAKVSCQGHNNLSLPCTFSQENOAETHAWFTSRFLYHVAGFLLPMLVNGWCY 238
 Db 181 LFLALPELLFAKVQGHNNLSLPCTFSQENOAETHAWFTSRFLYHVAGFLLPMLVNGWCY 240
 QY 239 VGVVHRLQORPQOKAVRVAILVTSIFFLCWSPHIVFDLTLARLKAVDNTCKLNG 298
 Db 241 VGVVHRLQORPQOKAVRVAILVTSIFFLCWSPHIVFDLTLERLKAIVNSSELG 300
 QY 299 SLPVAITMCBFLGLAHCLLPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRRS 358
 Db 301 YLSVAITLCEFFGLAHCLLPMPLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLFPSPWRRS 360
 QY 359 SLSESENATSLTTF 372
 Db 361 SLSESENATSLTTF 374
 RESULT 3
 ID CCR5_MOUSE STANDARD; PRT; 374 AA.
 AC 004683;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-X-C chemokine receptor type 5 (CXCR-5) (CXCR-5) (Burkitt's lymphoma receptor 1 homolog).
 GN Names=BLR1; Synonyms=Cxcr5, Gpcr6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RX MEDLINE=94009211; PubMed=8405054;
 RA Kaiser E., Foerster R., Wolf I., Epenberger C., Kuehl W.M., Lipp M.;
 RT "The G protein-coupled receptor BLR1 is involved in murine B cell
 RL differentiation and is also expressed in neuronal tissues.";
 RN Eur. J. Immunol. 23:2532-2539(1993).
 RP SEQUENCE OF 151-269 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94116980; PubMed=8288218;
 RA Wilkie T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
 RA Copeland N.G., Jenkins N.A.;
 RT "Identification, chromosomal location, and genome organization of
 RL mammalian G-protein-coupled receptors.";
 RN Genomics 18:175-184(1993).
 RN [3]
 RN CHARACTERIZATION.
 RX MEDLINE=97133211; PubMed=8978608; DOI=10.1016/S0092-8674(00)81798-5;
 RA Foerster R., Mattis A.E., Kremmer E., Wolf E., Brem G., Lipp M.;
 RT "A putative chemokine receptor, BLR1, directs B cell migration to
 RL defined lymphoid organs and specific anatomic compartments of the
 RN spleen.";
 RL Cell 87:1037-1047(1996).
 RN [4]
 RN LIGAND BINDING.
 RX MEDLINE=98146056; PubMed=9486651; DOI=10.1038/35876;
 RA Gunn M.D., Ngo V.N., Ansel K.M., Ekland E.H., Cyster J.G.,
 RA Williams L.T.;

RT "A B-cell-homing chemokine made in lymphoid follicles activates
 RT Burkitt's lymphoma receptor-1.";
 RL Nature 391:799-803(1998).
 CC -!- FUNCTION: Cytokine receptor that binds to B lymphocyte
 CC chemoattractant (BLC). Involved in B-cell migration into B-cell
 CC follicles of spleen and Peyer's patches, but not in those of
 CC mesenteric or peripheral lymph nodes.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Mainly in spleen, in resting B-cells.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; X71788; CAA50673.1; -;
 DR EMBL; L20332; AAA16852.1; -;
 DR PIR; S42628; S42628.
 DR MGI; MGI:103567; BLR1.
 DR InterPro; IPR000248; Angtn2_receptor.
 DR InterPro; IPR001053; CXCR5_Receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00241; CXCR5_KINERS.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR B-cell activation; G-protein coupled receptor; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 57 Extracellular (Potential).
 FT TRANSMEM 58 78 1 (Potential).
 FT DOMAIN 79 90 Cytoplasmic (Potential).
 FT TRANSMEM 91 111 2 (Potential).
 FT DOMAIN 112 126 Extracellular (Potential).
 FT TRANSMEM 127 147 3 (Potential).
 FT DOMAIN 148 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 190 4 (Potential).
 FT DOMAIN 191 221 Extracellular (Potential).
 FT TRANSMEM 222 242 5 (Potential).
 FT DOMAIN 243 261 Cytoplasmic (Potential).
 FT TRANSMEM 262 282 6 (Potential).
 FT DOMAIN 283 306 Extracellular (Potential).
 FT TRANSMEM 307 327 7 (Potential).
 FT DOMAIN 328 374 Cytoplasmic (Potential).
 FT CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).
 FT DISULFID 124 204 Potential.
 SQ SEQUENCE 374 AA; 42100 MW; 385258420C1EDE30 CRC64;
 Query Match 83.7%; Score 1635; DB 1; Length 374;
 Best Local Similarity 82.9%; Pred. No. 7.1e-104;
 Matches 310; Conservative 29; Mismatches 33; Indels 2; Gaps 1;
 QY 1 MNYPLTLEMD--LENLEDFWELDRDLNNDYNTSLVENHLCPCATGELMASFKAVFVPVAY 58
 Db 1 MNYPLTLDGMSITYNDDLYKELAFYSNSTEIFLQDSNFCSTVEGELLTSFKAVFVPVAY 60
 QY 59 SLIFLLGVGNVLVLILERHRTSRSTETFLFHLAVADLLVFLPFAVAESGVGWLG 118
 Db 61 SLIFLLGMGNILVLILERHRTSRSTETFLFHLAVADLLVFLPFAVAESGVGWLG 120
 QY 119 TFLCKTVIALKHVNFYCSSLLACIADVRYLAIVHAVYHRRLLSIHTCTIWLGVF 178
 Db 121 TFLCKTVIALKHNFYCSSLLACIADVRYLAIVHAVYHRRLLSIHTCTIWLGVF 180
 QY 179 LLALPEILPAKVSCQGHNNLSLPCTFSQENOAETHAWFTSRFLYHVAGFLLPMLVNGWCY 238
 Db 181 LFLALPELLFAKVQGHNNLSLPCTFSQENOAETHAWFTSRFLYHVAGFLLPMLVNGWCY 240

DR	InterPro: IPR001053; CXCL5_receptor.	DR	InterPro: IPR000276; GPCR_Rhodopsin.
DR	Fram; FR00001; 7tm_1; 1.	DR	Fram; FR00001; 7tm_1; 1.
DR	PRINTS; PR00657; CCCHMOKINER.	DR	PRINTS; PR00657; CCCHMOKINER.
DR	PRINTS; PR00564; CCCHMOKINERS.	DR	PRINTS; PR01532; CXCHMOKINER3.
DR	PRINTS; PR00237; GPCRHHODOPNS.	DR	PRINTS; PR00237; GPCRHHODOPNS.
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_1; 1.	DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.	DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW	Receptor.	KW	G-protein coupled receptor; Receptor; Transmembrane.
SQ	SEQUENCE 392 AA; 44760 MW; 3B5CFCE88366F088 CRC64;	SQ	SEQUENCE 366 AA; 40870 MW; 22AE9D136E09C0F CRC64;
Query Match			
Best Local Similarity 44.4%; Score 866.5; DB 2; Length 392;			
Matches 169; Conservative 57; Mismatches 116; Indels 7; Gaps 3;			
QY	28 NDTSLVENHLCPEATEGLMAS-----EKAVFPVVAYSLIFFLVGVGNVLVILVILRHQRTR 83	QY	34 ENHLC---PATEGPIMASFKAVFPVVAYSLIFFLVGVGNVLVILVILRHQRTRSTETFL 90
DB	47 NTPPSLEGVFCFNPSSILWLANQRDPKVFIPILAYILMFVLTGVQNALVLVILRPFKR 106	DB	31 ETYFCTSPPCQDPQSLNFDRTFLFVLYSLFLVLGLLGVVAVVLLSQRALSLSTDTFL 90
QY	84 STETELFLHADVADLLVFLPFAVEGSGVGLTFLCKVTYALHKVNFYCSSLLLACI 143	QY	91 FHLVADALLVFLPFAVEGSGVGLTFLCKVTYALHKVNFYCSSLLLACIADRYLA 150
DB	107 TTENFELFHLTLANALLTTFPSVVSLEAGWVFGTFLCKILSAVHKINFYLHEHAAGLH 166	DB	91 LHLVADALLVLTPLMVAADAIOHVFGSLCKVAGALFNIFYAGALLLACISFDRLS 150
QY	144 ADVRYLAIVHAYVHRRLLSIHITCGTIVLGVFLPALPEILFAKVSQGHNNSLPCT 203	QY	151 IVHAYVHRRLLSIHITCGTIVLGVFLPALPEILFAKVSQGHNNSL--PRCTFSQEN 208
DB	167 RVDRYLAIVYATYRKARSILHCTAIWLSLLTLPDLFMEVWTDENRSI--CY 224	DB	151 IVHATQFYRGPAPARVALTCVAVMGLCLFALPDFIFL---SSHDNRLNATHCQNPQ 207
QY	204 FSOENQAEHTAWFTSFLYHVAAGFLPMLVMGCVGVVHRLRQAORRQKAVRVAIL 263	QY	209 QAEHTAWFTSFLYHVAAGFLPMLVMGCVGVVHRLRQAORRQKAVRVAILVTSIF 268
DB	225 FPEAGIHGNVNLATFLYHVGFFPMLVMVCYMAIVRTLQSQRL--QRQKAVRVAIL 283	DB	208 EGRT----ALRVQLVAGFLPLLVMAICYARILTVL--LVSRGQRRLRAMRLVVVVVAF 262
QY	264 VTSIFPLCSPHIVIFLDTLARKAVDNTCKLNGSLPVAITWCPEFLGLAHCLNPLMT 323	QY	269 FLCWSPHIVIFLDTLARKAVDNTCKLNGSLPVAITWCPEFLGLAHCLNPLMTFAGVK 328
DB	284 VTGVFLCSPHIVIFLNTLTKLEAFKDCLEDHLDTAIMVTEAIGFTHCLNPIIYA 343	DB	263 ALCWTPYHLVVLVDTLMDLALARNCGRESVDVAKSVTSGMGYNHCLNPLLVAVGVK 322
QY	324 FGVKFRSRLTLTKLGCTGSPASLCQFPSSRRSSLSSESNATSLTTF 372	QY	329 FRSDLSRLTLTKLGCTG-----PASLCQFPSSRRSSLSSESNAT 367
DB	344 FGVKFRSRLTLTKLGCTGSPASLCQFPSSRRSSLSSESNATSLTTF 392	DB	323 FRKRWLLMRGLGCPDQGHORQPSA-----SRDSSWSWSETTEAS 362
RESULT 6			
Q867B2	PRELIMINARY; PRT; 366 AA.	Q6GNE2	PRELIMINARY; PRT; 390 AA.
AC	Q867B2;	AC	Q6GNE2;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)	DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)	DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	CXC chemokine receptor 3.	DE	LOC443669 protein (Fragment).
GN	Name=cxcr3;	GN	Name=LOC443669;
OS	Capra hircus (Goat).	OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC	Caprinae; Capra.	OC	Xenopodinae; Xenopus.
OX	NCBI_TaxID=9925;	OX	NCBI_TaxID=8355;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RX	MEDLINE=22765629; PubMed=12756249; DOI=10.1074/jbc.M300470200;	RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603889;
RA	Nagao K., Nollima H., Watanabe F., Chang K.T., Christenson R.K.,	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Sakai S., Imakawa K.	RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RT	"Regulation of Blastocyst Migration, Apposition, and Initial Adhesion	RA	Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RT	by a Chemokine, Interferon (gamma)-inducible Protein 10 kDa (IP-10),	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RT	during Early Gestation."	RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RL	J. Biol. Chem. 278:29048-29056(2003).	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC	- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
CC	- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.	RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
DR	EMBL; AB098893; BC55184.1;	RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
DR	GO; GO:0016021; C:integral to membrane; IEA.	RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
DR	GO; GO:0016493; F:C-C chemokine receptor activity; IEA.	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
DR	GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.	RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
DR	GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
DR	InterPro: IPR000355; Chmkin_receptor.	RA	InterPro: IPR000355; Chmkin_receptor.
DR	InterPro: IPR004070; CXCL5_receptor.	RA	InterPro: IPR004070; CXCL5_receptor.

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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RN SEQUENCE FROM N.A.
RN TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073571; AAH73571.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000355; Cmmkine receptor.
DR InterPro; IPR004070; CXCR3 receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01532; CXCCHUNKINER3.
DR PRINTS; PR00237; GPCRHOPOSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G PROTEIN RECEPTOR_F1_2; 1.
FT NON TER
SQ SEQUENCE 390 AA; 44470 MW; 44294060B6DCA92D CRC64;

* Query Match 32.7%; Score 638.5; DB 2; Length 390;
* Best Local Similarity 39.8%; Pred. No. 7.6e-36;
* Matches 130; Conservative 64; Mismatches 118; Indels 15; Gaps 5;

QY 49 FKAVFVPVAYSLFLGLGVGNVLVILRHQRTRSTETFLHLAVADLLVFLPFAV 108
DB 67 FDRFLPAFYSIVFLGLGMGNVLVLLQNRWLQSTDFLHLALADLLVVTLPFWA 126

QY 109 AEGSVGVGLTFFLCKTIALHKNFYCSSLLLACIADVRYLAIVHAYHRRLLSIHI 168
DB 127 TQAVSGWIFGNVLCKWVASIFKINFYACTFLVCISCDRLSVIYVQLYKKHRTLHVH 186

QY 169 TCGTIVLWFLPALPEILFAKVSQGHNSLPRCTFS-----QENQAETHAWFTS-RPLYH 223
DB 187 SCLLVVCLCIGLSIPDMVYRVTYE-----PRANVTDCQDFGHLDSKTWKISLTLVXH 240

QY 224 VAGFLPMLVMGCVGVVHRLQAQRPRQKAVRVAILVTSIFFLCWSPXHIVFLDT 283
DB 241 IVGFLIPLCFMVYCYTHIIHSLQTHGF-KKQKALRVVIAVWVIFLCWTFPYINVALD 299

QY 284 LARLKAVDNCKLNGSLPVAITMCEFLGLAHCCINPMLYTFAGVKFSDLSRLTLKGLCT 343
DB 300 MNLNLVLPDNCNTDSNIDIALSVTSGLCYFHSCLNPLLYAFVGAQPKQKLVLLNKLSCI 359

QY 344 GPASLQCLF---PSWRSSLSSESNAT 367
DB 360 CPQIVKKYIKYNPPAKPSTWSESGDTT 386

RESULT 8
CCR3 HUMAN STANDARD; PRT; 368 AA.
ID CCR3 HUMAN
AC P496B2; O15185; O9P2T4; O9P2T5;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-3) (CXCR-3) (CCR-L2) (CD183)

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DE antigen).
GN Name=CCR3; Synonyms=GPR9;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=97188912; PubMed=9064356;
RA Loetscher M., Gerber B., Loetscher P., Jones S.A., Piali L.,
RA Clark-Lewis I., Baggiolini M., Moser B.;
RT "Chemokine receptor specific for IP10 and mig: structure, function,
RT and expression in activated T-lymphocytes.";
RL J. Exp. Med. 184:963-969(1996).
RN [2]
RN SEQUENCE FROM N.A.
RA Gutierrez J., Varona R., Zaballo A., Lind P., Marquez G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain, Lung, and Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Pange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RN SEQUENCE OF 5-368 FROM N.A.
RX MEDLINE=96115583; PubMed=8666380;
RA Marchese A., Heiber M., Nguyen T., Heng H.H.Q., Saidi V.R.,
RA Cheng R., Murphy P.M., Tsui L.-C., Shi X., Gregor P., George S.R.,
RA O'Dowd B.F., Docherty J.M.;
RT "Cloning and chromosomal mapping of three novel genes, GPR9, GPR10,
RT and GPR14, encoding receptors related to interleukin 8, neuropeptide
RT Y, and somatostatin receptors.";
RL Genomics 29:335-344(1995).
RN [6]
RN SEQUENCE OF 278-368 FROM N.A., AND VARIANTS GLN-292 AND THR-363.
RX MEDLINE=21040285; PubMed=1196695; DOI=10.1038/sj.Gene.6363682;
RA Kato H., Tsuchiya N., Tokunaga K.;
RT "Single nucleotide polymorphisms in the coding regions of human CXCR-
RT chemokine receptors CXCR1, CXCR2 and CXCR3.";
RL Genes Immun. 1:330-337(2000).
RN [7]
RN LIGAND BINDING.
RC TISSUE=Fetal astrocytes;
RX MEDLINE=98290735; PubMed=9625760;
RA Cole K.E., Strick C.A., Paradis T.J., Ogborne K.T., Loetscher M.,
RA Gladue R.P., Lin W., Boyd J.G., Moser B., Wood D.E., Sahagan B.G.,
RA Neote K.;

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RT "Interferon-inducible T cell alpha chemoattractant (I-TAC): a novel
 RT non-ELR CXCL chemokine with potent activity on activated T cells
 RL through selective high affinity binding to CXCR3.";
 J. Exp. Med. 187:2009-2021(1998).
 CC -1- FUNCTION: Receptor for SCYB9/MIG, SCYB10/INP10 and SCYB11/ITAC.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 1:78-83(2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/650534941_g.htm".
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X95876; CAA65126.1; --
 DR EMBL; Z79783; CAB02143.1; ALT_INIT.
 DR EMBL; AY242128; AAC92295.1; --
 DR EMBL; BC034403; AAH34403.1; --
 DR EMBL; U32674; AAC50505.1; --
 DR EMBL; AB032735; BAA92297.1; --
 DR EMBL; AB032736; BAA92298.1; --
 DR GenBank; HGNC:4540; CXCR3.
 DR H-invDB; HIX0016864; --
 DR MIM; 600894; --
 DR GO; GO:0005737; C:cytoplasm; TAS.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004950; F:chemokine receptor activity; TAS.
 DR GO; GO:0019735; P:antimicrobial humoral response (sensu Verte. . .); TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0006935; P:chemotaxis; TAS.
 DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
 DR InterPro; IPR000355; Chkline_receptor.
 DR InterPro; IPR004070; CXCL_3_receptor.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PR01532; KCCHMKINER3.
 DR PRINTS; PR00237; GPCR_RHODPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Antigen; G-protein coupled receptor; Glycoprotein; Polymorphism;
 KW Transmembrane.
 FT DOMAIN 1 53 Extracellular (Potential).
 FT TRANSMEM 54 80 1 (Potential).
 FT DOMAIN 81 89 Cytoplasmic (Potential).
 FT TRANSMEM 90 110 2 (Potential).
 FT DOMAIN 111 125 Extracellular (Potential).
 FT TRANSMEM 126 147 3 (Potential).
 FT DOMAIN 148 169 Cytoplasmic (Potential).
 FT TRANSMEM 170 189 4 (Potential).
 FT DOMAIN 190 212 Extracellular (Potential).
 FT TRANSMEM 213 233 5 (Potential).
 FT DOMAIN 234 255 Cytoplasmic (Potential).
 FT TRANSMEM 256 277 6 (Potential).
 FT DOMAIN 278 298 Extracellular (Potential).
 FT TRANSMEM 299 321 7 (Potential).
 FT DOMAIN 322 368 Cytoplasmic (Potential).
 FT DISULFID 124 203 By similarity.
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 32 32 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 292 292 R -> Q.
 FT VARIANT 363 363 A -> T.
 FT CONFLICT 75 75 A -> R (in Ref. 2).
 FT SEQUENCE 368 AA; 40659 MW; F08A3B44B2BBAD04 CRC64;
 SQ
 Query Match 32.5%; Score 635; DB 1; Length 368;
 Best Local Similarity 40.8%; Pred. No. 1.3e-35;

Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
 QY 11 LENLEDLFWELDRLDNYNDTSLVNHLCPATEGLPMASFKAVFPVAVYSLIFLLGVGNV 70
 DB LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLGLGNG 72
 QY 71 LVLVILERHQRTRSTETFLHLAVADLLLVFILPFAVAGSVGVWLTGFLCKTVALHK 130
 DB 73 AVAAVLLSRRRTALSTDTFLHLAVADTLVLTLPMAVDAVQWVFGSGCLKVAGALFN 132
 QY 131 VNFYCSLLACIAVDRIALIVHVAHVHRELLSHITCGTIWLVGFLALPEILFAKV 190
 DB 133 INFYAGALLACISFDRIYLVHATQLYRGGPARVTLTCLAVMGICLLFALPDPFL-- 190
 QY 191 SOGHNNLS--PRCTFSQENQAEATHAFTSRFLYHVAGFLPMLVMGVCYGVVHRLQA 248
 DB 191 -SAHDERLNATHCOYNFPQVGR-----ALRVQLVAGVFLPLLVNAYCAHILAVL-LV 244
 QY 249 QRRPQOKAVRVAIIIVTSIFFLCWSPHYHIVFLDTLARLKAVDNTCKLNSLPVAITMCE 308
 DB 245 SRGQRLRAMRLVVVVVAFALCWTFFHLVLDVLDLMDLGALARNCGRESRVDVAKSVTS 304
 QY 309 FLGLAHCCINPMLYTFAGVKFRSDLSRLITKLGCTGPASLCOFPSPWRR--SSLSESENAT 367
 DB 305 GLGYMHCCINPLLYAFVGVKFRERMMWMLLRLLGCPNQRLQRPSSSRDSSWSETSEAS 364
 RESULT 9
 Q72710 PRELIMINARY; PRT; 415 AA.
 ID Q72710
 AC Q72710
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CXCL chemokine receptor transcript variant B.
 GN Name=GPR9;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22666871; PubMed=12782716;
 RA Laesagni L., Francalanci M., Annunziato F., Lazzeri E., Giannini S.,
 RA Cosmi L., Sagrinati C., Mazzinghi B., Orlando C., Maggi E., Marra F.,
 RA Romagnani S., Serio M., Romagnani P.;
 RT "An alternatively spliced variant of CXCR3 mediates the inhibition of
 RT endothelial cell growth induced by IP-10, Mig, and I-TAC, and acts as
 RT functional receptor for platelet factor 4.";
 RL J. Exp. Med. 197;1537-1549(2003).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF469635; AAP55851.1; --
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 415 AA; 45522 MW; 325C8A65982A43C4 CRC64;
 Query Match 32.5%; Score 635; DB 2; Length 415;
 Best Local Similarity 40.8%; Pred. No. 1.4e-35;
 Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
 QY 11 LENLEDLFWELDRLDNYNDTSLVNHLCPATEGLPMASFKAVFPVAVYSLIFLLGVGNV 70
 DB LENFSSSY---DYGENESD-SCCTSPPCPQ---DFSLNFDRAFLPALYSLLFLGLGNG 119
 QY 71 LVLVILERHQRTRSTETFLHLAVADLLLVFILPFAVAGSVGVWLTGFLCKTVALHK 130

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Db 120 AVAAVLLSRRTALSTDTFLHLAVADTLVTLPLWADVAQVQVFGSLCKVAGALFN 179
QY 131 VNFVCSLLLACIAVDYLAIVHVAHYRRLLSIHITCGTTLVGLFLLALPEILFAKV 190
Db 180 INFVAGALLIACISFDRIYLVHATQYRGRGPPARVTLTCLAVGICLLFALPDFL-- 237
QY 191 SQGHNNLSL--PRCTFSQENQAETHAWFTSRFLVHAGFLPMLVMGWCYGVVHRLRQA 248
Db 238 -SAHDERLNATHCOYVFPQVGR-----ALRVQLVAGFLPLLVMAICYAHILAVL-LV 291
QY 249 QRAPQOKAVRAVAILVTSIFFLCWSPHIVFLDTLRLKAVDNTCKLNGSLPVAITMCE 308
Db 292 SRGQRRLRARVRLVVVVVAFALCWTPYHLVVLVDILMDLGALARNCGRESKRVDAKSVTS 351
QY 309 FLGLAHCLNPMPLVTFAGVFRSRLSLTLKLGCTGPASLCOLFPSPWRR--SSLSEGENAT 367
Db 352 GLGYMHCLLAPLLYAFVGVFRERMMWLLRLGCPNORGLQRQPSRRRDSWSSETSEAS 411
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RESULT 10

Q9QWN6 PRELIMINARY; PRT; 367 AA.

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AC Q9QWN6;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Interferon-inducible protein 10 receptor.
GN Name=Cxcr3; Synonyms=Cxcr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=99009219; PubMed=9790904; DOI=10.1006/bbrc.1998.9404;
RA Tamari M., Tomimaga Y., Yatsunami K., Narumi S.;
RT "Cloning of the murine interferon-inducible protein 10 (IP-10)
RL receptor and its specific expression in lymphoid organs.";
RL Biochem. Biophys. Res. Commun. 251:41-48(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB003174; BAA34045.1; -.
DR PIR; JEO349; JEO349.
DR MGD; MGI:1277207; Cxcr3.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR004070; CX3_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CXCCHMKINER.
DR PRINTS; PR01532; CXCCHMKINER3.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 41017 MW; EF0348A8358AD951 CRC64;
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Query Match 31.5%; Score 615; DB 2; Length 367;
Best Local Similarity 38.8%; Pred. No. 2.9e-34;
Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;

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QY 28 NDTSLVENHLCPATEGLPMASFAKAVFVPAVSGVGLTGLCKTVIALHKVNFYCSSLLIACIADV 87
Db 32 NESDFSDSPCPQ---DFSLNFORTFALYSLFLGLLGNAGVAAVLISQRTALSST 88
QY 88 TELFLHVAADLLVFLPFAVAGSGVGLTGLCKTVIALHKVNFYCSSLLIACIADV 147
Db 89 TELFLHVAADLLVTLPLWADVAQVQVFGSLCKVAGALFNINFVAGFLACISFDR 148
QY 148 YLAIVHVAHYRRLLSIHITCGTTLVGLFLLALPEILFAKVSGQHHNLSLPRCTFSQE 207
```

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Db 149 YLSIVHATQIYRRDRPRVRVALTCIVVGLCLLFFALPDFIYLSANYDQRLNA-THCQNF 207
QY 208 NOAETHAWFTSRFLVHAGFLPMLVMGWCYGVVHRLRQAQRPRQKAVRAVAILVTSI 267
Db 208 QVGR-----ALRVQLVAGFLPLLVMAICYAHILAVL-LVSRGQRFRAMRLVVVVAA 262
QY 268 PFLCWSPHIVFLDTLRLKAVDNTCKLNGSLPVAITMCEFLGLAHCLNPMPLVTFAGV 327
Db 263 FAVCWTPYHLVVLVDILMDVGLARNCGRESKRVDAKSVTSQVGMVHCHCLNPLLYAFVGV 322
QY 328 KFRSRLSLTLKLGCT---GPASLCOLFPSPWRRSSLSSEGENATSL 369
Db 323 KFRQWMLFTRLGRSDQRPOR--QPSSSRRESSWSETSEAYL 365
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RESULT 11

CCR3_MOUSE STANDARD; PRT; 367 AA.

AC C88410;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-X-C chemokine receptor type 3 (CXCR-R3) (CXCR-3).
GN Name=Cxcr3; Synonyms=Cxcr3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=981836; PubMed=9653165; DOI=10.1073/pnas.95.14.8205;
RA Soto H., Wang W., Strieter R.M., Copeland N.G., Gilbert D.J.,
RA Jenkins N.A., Hedrick J., Zlotnik A.;
RT "The CC chemokine 6CKine binds the CX3 chemokine receptor CXCR3.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8205-8210(1998).
CC -1- FUNCTION: Receptor for SCYB9/MTG, SCYB10/INP10 and SCYB11/ITAC (By similarity). Binds to SCYB1.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC EMBL; AF045146; AAC40163.1; -.
DR MGD; MGI:1277207; Cxcr3.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR004070; CX3_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01532; CXCCHMKINER3.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Transmembrane.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 52
FT TRANSMEM 53 79
FT DOMAIN 80 88
FT TRANSMEM 89 109
FT DOMAIN 110 124
FT TRANSMEM 125 146
FT DOMAIN 147 168
FT TRANSMEM 169 188
FT DOMAIN 189 211
FT TRANSMEM 212 232
FT DOMAIN 233 254
FT TRANSMEM 255 276
FT DOMAIN 277 297
FT TRANSMEM 298 320


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FT DOMAIN 321 367 Cytoplasmic (Potential).
FT DISULFID 123 202 By similarity.
FT CARBOHYD 22 22 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 32 32 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 367 AA; 41016 MW; 029FBB778E3CD4EA CRC64;

Query Match 31.4%; Score 614; DB 1; Length 367;
Best Local Similarity 38.8%; Pred. No. 3.4e-34;
Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;

QY 28 NDTSLVENHLCPEGELMASFKAVFVPVAYSLIFLLGVIGNVLVILVILERHRTSRSTE 87
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 32 NESDFSPPCPQ---DFSINFDRTFLPVLYSLLFLGLGNGAVALLSQRTALSSTD 88
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 88 TFLHLAVADLLVFLPFAVAGSGVWLTGTFCKTVIALHKVNFYCSSLLACIAVDR 147
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 89 TFLHLAVADVLLVTLPLWADVAQVWFGGLCKVAGALENFYAGAFLLACISFDR 148
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 148 YLAIVHAVHAYRHRRLSLIHTCTIWLGVFLLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 207
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 149 YLSIVHATQIYRRDPVRVVALTCIVWGLCLLFPALDFIYLSANYDQRLNA-THCQYNFP 207
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 208 NOAETHAWFTSRFLYHVAGFLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 267
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 208 QVGR-----ALRVQLVAGFLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 267
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 268 FFLCWSPIHIVIFLDTLRLKAVDNTCKLNGSLPVAITMCEFLGLAHCCCLNPMMLYTFAGV 327
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 263 FAVCWTPYHLVLDVILMDVGLARNCGRSHVDVAKSVTSGMGYHCCCLNPLLYAFVGV 322
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 328 KFRSDLSRLTLKLGCT---GPASLCQLFPSPWRSSISESENATSL 369
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 323 KPREKMMMLFRLGRSDQRPQR--QPSSRRSSSWSETTEASYL 365

RESULT 12
Q9JII9 PRELIMINARY; PRT; 367 AA.
ID Q9JII9
AC Q9JII9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Chemokine receptor CXCR3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20286573; PubMed=10825390;
RA Wang X., Li X., Schmidt D.B., Foley J.J., Barone F.C., Ames R.S.,
RA Sarau H.M.;
RT "Identification and molecular characterization of rat CXCR3: receptor
RT expression and interferon-inducible protein-10 binding are increased
RT in focal stroke.";
RL Mol. Pharmacol. 57:1190-1198 (2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL, AF223642; AAF76982.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor activity; IEA.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR004070; CXCR3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01532; CXCHMKINER3.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
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DR PROSITE; PSS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 367 AA; 40934 MW; F67C0362EDDBFCB7 CRC64;

Query Match 31.4%; Score 613; DB 2; Length 367;
Best Local Similarity 38.8%; Pred. No. 4e-34;
Matches 134; Conservative 58; Mismatches 139; Indels 14; Gaps 6;

QY 28 NDTSLVENHLCPEGELMASFKAVFVPVAYSLIFLLGVIGNVLVILVILERHRTSRSTE 87
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 32 NESDFSPPCPQ---DFSINFDRTFLPVLYSLLFLGLGNGAVALLSQRTALSSTD 88
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 88 TFLHLAVADLLVFLPFAVAGSGVWLTGTFCKTVIALHKVNFYCSSLLACIAVDR 147
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 89 TFLHLAVADVLLVTLPLWADVAQVWFGGLCKVAGALENFYAGAFLLACISFDR 148
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 148 YLAIVHAVHAYRHRRLSLIHTCTIWLGVFLLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 207
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 149 YLSIVHATQIYRRDPVRVVALTCIVWGLCVLFPALDFIYLSASHQRLNA-THCQYNFP 207
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 208 NOAETHAWFTSRFLYHVAGFLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 267
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 208 QVGR-----ALRVQLVAGFLPMLVGMVGVVHRLRQAPRQOKAVRVAILVTSI 267
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 268 FFLCWSPIHIVIFLDTLRLKAVDNTCKLNGSLPVAITMCEFLGLAHCCCLNPMMLYTFAGV 327
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 263 FAVCWTPYHLVLDVILMDVGLARNCGRSHVDVAKSVTSGMGYHCCCLNPLLYAFVGV 322
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
QY 328 KFRSDLSRLTLKLGCT---GPASLCQLFPSPWRSSISESENATSL 369
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 323 KPREKMMMLFRLGRSDQRPQR--QPSSRRSSSWSETTEASYL 365

RESULT 13
Q802H1 PRELIMINARY; PRT; 374 AA.
ID Q802H1
AC Q802H1
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine receptor CXCR4.
GN Name=CXCR4;
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22557679; PubMed=12671740;
RA Kuroda N., Uinuk-Cool T.S., Sato A., Samonte I.E., Figueroa F.,
RA Mayer W.E., Klein J.;
RT "Identification of chemokines and a chemokine receptor in cichlid
RT fish, shark, and lamprey.";
RL Immunogenetics 54:884-895 (2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY178969; AAO21209.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004945; F:angiogenesis type II receptor activity; IEA.
DR GO; GO:0016494; F:C-X-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
DR InterPro; IPR000248; Angtn2_receptor.
DR InterPro; IPR001277; GPCR_4_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00241; ANGIOTENSINR.
DR PRINTS; PR00645; CXCHMKINER4.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
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SQ SEQUENCE 374 AA; 41113 MW; DEBD92B366776A0D CRC64;
 Query Match 31.1%; Score 607; DB 2; Length 374;
 Best Local Similarity 40.2%; Pred. No. 1e-33;
 Matches 137; Conservative 55; Mismatches 123; Indels 26; Gaps 9;
 QY 21 LDRLD-----NYNDTS-LVENHLCPCATEGPL-----MASFKAVFVPVAVSLIFLLGVGNVL 71
 DB 10 LDEADLLPMGLNDTSELDNPPRPAATAPTCLAPSQSFHRVFLPVVYGLVCLLLGFAGNGL 69
 QY 72 VLVILHRHQRSTRSTETFLHLAVADLLVFLPFAVAGSVGWLTGFLCKTVIALHKV 131
 DB 70 ILVLTCTKXTSSDYLMLHAADLLFLVTFWAVGSAATEKVFNGVLCCLVNFVTFV 129
 QY 132 NFYCSSLACIAVDRLAIHVAHVHRRRLLSIHITCGTIVLGVFLALPEILPAKV- 190
 DB 130 NLASSILLACISIERVLAIVRATKDKVRKPKATKVTCCAVWALSLLAMPDLVESHVY 189
 QY 191 ---SQGHH--NNSLPRCTFSQENOAETHAWFTS--RFLYHVAGFLPMLVWGVCYGVVHR 244
 DB 190 IAPLSGHOLCEHVVP-----ESASELWRTSLRALHHLAFALPGIVIVFCVMVIRT 241
 QY 245 LRQQRPRQKAVRVAILVTSIFFLCWSPHYHIVFDLTARLKAVDNT--CKLNGSLPVA 303
 DB 242 LSQLNHH-ERKALKVVVAIAAFAFFVCWLPYNNVVTLLDTRMLDVAVNSDCMEQR LGVA 300
 QY 304 ITWCEPLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTG 344
 DB 301 VAVTEGVGFSHCCPIPVYAFVGKFKENLARLNGCKACVG 341

RESULT 14

Q8HZN4 PRELIMINARY; PRT; 355 AA.
 AC Q8HZN4
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 8 receptor B CXCR2.
 OS Cercopithecus pygerythrus (Vervet monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Cercopithecus.
 OC NCBI_TaxID=60710;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B.,
 RA Baldwin J.J., Auld D.S.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF540793; AANL7319.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004918; F:interleukin-8 receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000057; IL8B_receptor.
 DR InterPro; IPR000174; IL8_Receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 355 AA; 40381 MW; D464957687BBFBFC CRC64;

Query Match 31.0%; Score 606; DB 2; Length 355;
 Best Local Similarity 39.0%; Pred. No. 1.2e-33;
 Matches 142; Conservative 54; Mismatches 156; Indels 12; Gaps 8;

QY 9 MDLENLEDFWELDRDNDYNTSLVENHLCPCATE-GPLMASFKAVFVPVAVSLIFLLGVI 67
 DB 1 MEISNFEDL-WKSEDFSNYSYSSDLPPSLPDVTPCRPESLEINKYFWIYIYALVFLLSLL 59
 QY 68 GNVLVVLILHRHQRSTRSTETFLHLAVADLLVFLPFAVAGSVGWLTGFLCKTVIA 127
 DB 60 GNSLVMLVTLHRSVGRSVTDVYLLNLAMADLAFALTLPITWAAAKQNGWIFGTFLCKVSL 119
 QY 128 LHKVNFYCSLLACIAVDRLAIHVAHVHRRRLLSIHITCGTIVLGVFLALPEILF 187
 DB 120 LKVNPFYSILLACISVDRLAIHVAHTLTQKRYL-VKFCVLSIWGLSLLALPVLFL 178
 QY 188 AKVSGQHNNSLPRCTFSQENOAETHAW-FTSRFLYHVAGFLPMLVWGVCYGVVHRLR 246
 DB 179 RRTVPTYIS--PVCYEDMGN--NTAKWRMLRILPQTGFILPLLIMLFCYGTTLTLF 234
 QY 247 QQRPRQKAVRVAILVTSIFFLCWSPHYHIVFDLTARLKAVDNTCKLNGSLPVAITM 306
 DB 235 KA-HMGQKRAMRVIFAVVLIIFLLCWLPHYLVLLTDTLMRTLRKIKETCORRNDIDRALDA 293
 QY 307 CEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCOLPPSVRRSSLSSENA 366
 DB 294 TEILGLHSCLNPIIYAFIGQKFRHGLLKILATHGLISKDSLPK---DSRPFSVGSSEGH 350
 QY 367 TSLT 370
 DB 351 TSST 354

RESULT 15

Q8HZN8 PRELIMINARY; PRT; 355 AA.
 AC Q8HZN8
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Interleukin 8 receptor B CXCR2.
 OS Pan troglodytes (Chimpanzee).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Horlick R.A., Zhao J., Swanson R.N., Webb M.L., Strohl B.,
 RA Baldwin J.J., Auld D.S.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AF540789; AANL7315.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004918; F:interleukin-8 receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0006935; P:chemotaxis; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000057; IL8B_receptor.
 DR InterPro; IPR000174; IL8_Receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PRINTS; PR00427; INTRLEUKIN8R.
 DR PRINTS; PR00573; INTRLEUKIN8R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 355 AA; 40122 MW; 809AB63ADA6A42C6 CRC64;

Query Match 30.8%; Score 601.5; DB 2; Length 355;
 Best Local Similarity 38.6%; Pred. No. 2.4e-33;
 Matches 141; Conservative 57; Mismatches 154; Indels 13; Gaps 8;

QY 9 MDLENLEDFWELDRDNDYNTSLVENHLCPCATE-GPLMASFKAVFVPVAVSLIFLLGVI 67

Db	1	MESDSFED-FWKGEDLSNYSSTLPPFLDADCEPESLEINKYFVVIYALVFLLSLL	59
Qy	68	GNVLVLVILERRHROTRSTETFLPHLAVADLLVFIPLFAVAGSGVGLTFLCKTVIA	127
Db	60	GNLSVMLVILYSRVGRSVTDVYLLNLALADLLFALTLPWAASKVNGWIFGTFLCKVSL	119
Qy	128	LHKVNFYCSSLILLACIADVRLAIIVHAYHAYRHRLLSIHITCGTIWLVGFILLALPEILF	187
Db	120	LKEVNFYSGILLACISVDRYLAIVHATRTLTKRYL-VKFCISIWGLSLLALPVLLF	178
Qy	188	AKYSQGHNNLSLPRCTFSQENQAEHAW-FTSRFLYHVAGFLPMLVMGWCYGVVHRLR	246
Db	179	RRTV--YSSNVSPACYEDMGN--NTANWRMLLRLLPQSGFIVPELLIMLFCYGTTLTLF	234
Qy	247	QAQRRPQOKAVRVAILVTSIFFLCWSPHYHIVFLDTLARLKAVDNTCKLNGSLPVAITM	306
Db	235	KA-HMGQKHARMRVIFAVVLIFFLCWLPYNVLLADTLMTQVIOETCERRNHIDRALDA	293
Qy	307	CEFLGLAHCCINPMLYTFAGVKFRSDLSRLITKLGGTGPASLCQLPFSWRSSLSSENA	366
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Db	350	HTST 354	

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Job time : 176 secs

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QM protein - protein search, using sw model

Run on: August 29, 2005, 23:48:26 ; Search time 42 seconds
(without alignments)
661.177 Million cell updates/sec

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Perfect score: 1953
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*
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4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*
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6: /cgn2_6/prodata/1/iaa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1953	100.0	372	1	US-08-202-056-5
2	1953	100.0	372	1	US-08-076-093A-6
3	1953	100.0	372	1	US-08-701-265-6
4	1953	100.0	372	2	US-08-284-586-6
5	1953	100.0	372	2	US-08-805-478-6
6	1953	100.0	372	2	US-08-802-627A-6
7	1953	100.0	372	2	US-08-801-238-6
8	1953	100.0	372	2	US-08-801-228-6
9	1953	100.0	372	3	US-09-104-296-6
10	1953	100.0	372	3	US-08-982-493-8
11	1953	100.0	372	4	US-09-170-496D-66
12	1953	100.0	378	4	US-09-949-016-10255
13	1947	99.7	372	4	US-09-170-496D-200
14	1635	83.7	374	3	US-08-982-493-6
15	635	32.5	368	3	US-08-709-838-2
16	635	32.5	368	3	US-08-829-839-2
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19	635	32.5	368	4	US-09-607-156-2
20	632	32.4	368	4	US-09-170-496D-174
21	601.5	30.8	355	1	US-07-759-568-1
22	601.5	30.8	355	1	US-08-450-393A-8
23	601.5	30.8	355	2	US-08-390-000A-5
24	601.5	30.8	355	3	US-08-446-669-8
25	601.5	30.8	355	4	US-09-625-573-8
26	601.5	30.8	355	5	PCT-US95-00476-8
27	601.5	30.8	360	1	US-08-202-056-7

28 601.5 30.8 360 4 US-09-409-778-4 Sequence 4, Appli
29 596 30.5 358 1 US-08-153-848-19 Sequence 19, Appl
30 596 30.5 358 3 US-09-299-843A-19 Sequence 19, Appl
31 596 30.5 358 3 US-09-088-337B-19 Sequence 19, Appl
32 596 30.5 358 5 PCT-US93-11153-19 Sequence 19, Appl
33 596 30.5 378 1 US-08-153-848-15 Sequence 15, Appl
34 596 30.5 378 3 US-09-299-843A-15 Sequence 15, Appl
35 596 30.5 378 3 US-09-251-545-1 Sequence 1, Appl
36 596 30.5 378 3 US-09-088-337B-15 Sequence 15, Appl
37 596 30.5 378 4 US-09-170-496D-74 Sequence 74, Appl
38 596 30.5 378 5 PCT-US93-11153-15 Sequence 15, Appl
39 596 30.5 410 1 US-08-153-848-7 Sequence 7, Appl
40 596 30.5 410 3 US-09-299-843A-7 Sequence 7, Appl
41 596 30.5 410 3 US-09-088-337B-7 Sequence 7, Appl
42 596 30.5 410 5 PCT-US93-11153-7 Sequence 7, Appl
43 591 30.3 378 4 US-09-170-496D-204 Sequence 204, App
44 574 29.4 378 1 US-08-383-750-2 Sequence 2, Appli
45 574 29.4 378 1 US-08-383-751A-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-202-056-5
; Sequence 5, Application US/08202056
; Patent No. 5440021
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Hebert, Caroline
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Lee, James
; TITLE OF INVENTION: Antibodies to Human IL-8 Type B Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,056
; FILING DATE: 25-FEB-1994
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-202-056-5

Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
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Db 61 IFLLGVIGNVLVILERHROTSSSTETFLPHLAVADLLVFLPFAVAEGSVGWLGTF 120
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Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYRHRRLLSIHITCGTIWLVGFLL 180
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Db 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
Qy 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAORRQORQKAVRVAILVTSIFFLCWSPHYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLFPSWRRSSL 360
Db 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLFPSWRRSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 2

US-08-076-093A-6
; Sequence 6, Application US/08076093A
; Patent No. 5543503
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/076,093A
; FILING DATE: 11-Jun-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: 706P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid

; TOPOLOGY: Linear
US-08-076-093A-6
Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
Db 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
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Db 61 IFLLGVIGNVLVILERHROTSSSTETFLPHLAVADLLVFLPFAVAEGSVGWLGTF 120
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Db 121 LCKTVIALHKVNFYCSSLLACIAVDRLAI VHAHVAYRHRRLLSIHITCGTIWLVGFLL 180
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Db 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQCLFPSWRRSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 3

US-08-701-265-6
; Sequence 6, Application US/08701265
; Patent No. 5776457
; GENERAL INFORMATION:
; APPLICANT: Chuntharapai, Anan
; APPLICANT: Lee, James
; APPLICANT: Hebert, Caroline
; APPLICANT: Jin Kim, K.
; TITLE OF INVENTION: Antibodies to Human PF4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,265
; FILING DATE: 22-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-Jun-1993
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/677211
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B

REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-701-265-6

Query Match 100.0%; Score 1953; DB 1; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
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QY 241 VVHRLQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLAKLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLAKLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 4

US-08-284-586-6
Sequence 6, Application US/08284586
Patent No. 5840856
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: Antibodies to Human PF4A Receptors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,586
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/076,093A
FILING DATE: 11-Jun-1993
APPLICATION NUMBER: 07/810782
FILING DATE: 19-DEC-1991
PRIOR APPLICATION DATA: 07/677211
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 706P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-284-586-6

Query Match 100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFPVAYS 60
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DB 61 IFLLGVIGNVLVILERHQRTRSTETFLFLAVADLLVFLPFAVAEGSVGVLGTF 120
QY 121 LCKTVIALHKVNYCSSLACIADRYLAIVHAVHAYRHRLLSHITCGTIWLVGFLL 180
DB 121 LCKTVIALHKVNYCSSLACIADRYLAIVHAVHAYRHRLLSHITCGTIWLVGFLL 180
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DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHAWFTSRFLYHAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLAKLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRAVAILVTSIFFLCWSPYHIVFLDTLAKLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 5

US-08-805-478-6
Sequence 6, Application US/08805478
Patent No. 5874543
GENERAL INFORMATION:
APPLICANT: Chuntharapai, Anan
APPLICANT: Lee, James
APPLICANT: Hebert, Caroline
APPLICANT: Jin Kim, K.
TITLE OF INVENTION: ANTIBODIES TO PF4A RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

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; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,478
; FILING DATE: 25-Feb-1997
; CLASSIFICATION: 530
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; US-08-805-478-6
;
; Query Match 100.0%; Score 1953; DB 2; Length 372;
; Best Local Similarity 100.0%; Pred. No. 8.7e-176;
; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
; DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
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; DB 61 IFLLGVGNVLVLVILERHROTRSSSTETFLHLAVADLLLVFILPFAVAGSVGVVLGTF 120
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; QY 121 LCKTVIALHKVNFYCSSLILACIAVDRLYLAIHVAVHAYRHRLLSHITCGTIWLVGFL 180
; DB 121 LCKTVIALHKVNFYCSSLILACIAVDRLYLAIHVAVHAYRHRLLSHITCGTIWLVGFL 180
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; QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
; DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
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; QY 241 VVHLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
; DB 241 VVHLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
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; QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCOLFSPSWRRSSL 360
; DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCOLFSPSWRRSSL 360
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; QY 361 SESENATSLTTF 372
; DB 361 SESENATSLTTF 372

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RESULT 6

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US-08-802-627A-6
; Sequence 6, Application US/08802627A
; Patent No. 5892017
; GENERAL INFORMATION:
; APPLICANT: Lee, James

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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,627A
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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; US-08-802-627A-6
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; Query Match 100.0%; Score 1953; DB 2; Length 372;
; Best Local Similarity 100.0%; Pred. No. 8.7e-176;
; Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
; DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYS 60
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; QY 61 IFLLGVGNVLVLVILERHROTRSSSTETFLHLAVADLLLVFILPFAVAGSVGVVLGTF 120
; DB 61 IFLLGVGNVLVLVILERHROTRSSSTETFLHLAVADLLLVFILPFAVAGSVGVVLGTF 120
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; QY 121 LCKTVIALHKVNFYCSSLILACIAVDRLYLAIHVAVHAYRHRLLSHITCGTIWLVGFL 180
; DB 121 LCKTVIALHKVNFYCSSLILACIAVDRLYLAIHVAVHAYRHRLLSHITCGTIWLVGFL 180
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; QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
; DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAEHTAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
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; QY 241 VVHLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
; DB 241 VVHLRQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNCKLNSL 300
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; QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCOLFSPSWRRSSL 360
; DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLITKLGCTGPASLCOLFSPSWRRSSL 360
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; QY 361 SESENATSLTTF 372
; DB 361 SESENATSLTTF 372

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Db          361 SESENATSLTTF 372
RESULT 7
US-08-801-238-6
; Sequence 6, Application US/08801238
; Patent No. 5919896
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; TITLE OF INVENTION: PF4A RECEPTOR
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,238
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-238-6
Query Match          100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
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QY      61 IFLGVIGNVLVILERHQRTRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
Db      61 IFLGVIGNVLVILERHQRTRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
QY      121 LCKTVIALHKVNFYCSSLLACIADRYLAIYHVAHYHRRLLSIHITCGTIWLVGFL 180
Db      121 LCKTVIALHKVNFYCSSLLACIADRYLAIYHVAHYHRRLLSIHITCGTIWLVGFL 180
QY      181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAEHTAMFTSRFLYHAGVFLPMLVMGCVYG 240
Db      181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAEHTAMFTSRFLYHAGVFLPMLVMGCVYG 240
QY      241 VVHRLRQARRPQRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCKNGSL 300

Db          241 VVHRLRQARRPQRQKAVRVAILVTSIFFLCWSPHYHIVFLDTLARKAVDNTCKNGSL 300
QY          301 PVAITWCEFLGLAHCLNPLMYTFAGVKFRSDLSRLLTKLGGCTGPASLQCLPFSWRSSSL 360
Db          301 PVAITWCEFLGLAHCLNPLMYTFAGVKFRSDLSRLLTKLGGCTGPASLQCLPFSWRSSSL 360
QY          361 SESENATSLTTF 372
Db          361 SESENATSLTTF 372
RESULT 8
US-08-801-228-6
; Sequence 6, Application US/08801228
; Patent No. 5922541
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; TITLE OF INVENTION: METHODS FOR DETECTION AND AMPLIFICATION OF
; TITLE OF INVENTION: PF4A RECEPTOR NUCLEIC ACID
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,228
; FILING DATE: 19-Feb-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/284586
; FILING DATE: 10-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-801-228-6
Query Match          100.0%; Score 1953; DB 2; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
Db      1 MNYPLTLEMDLENLEDFWELDRDNDYNTSLVENHLCPCATEGPLMASFKAVFVPVAYSL 60
QY      61 IFLGVIGNVLVILERHQRTRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
Db      61 IFLGVIGNVLVILERHQRTRSTETFLFLAVADLLVFLPFAVAEGSVGVVLGTF 120
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Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRIYLAIVHAYHRRRLLSIHITCGTIWLVGFLL 180
Db 121 LCKTVIALHKVNFYCSSLLACIAVDRIYLAIVHAYHRRRLLSIHITCGTIWLVGFLL 180
Qy 181 ALPEILFAKVSQGHNNLSLPRCTFSEQNOAETHAWFTSRFLYHAGFLLPMLVWGVCYVG 240
Db 181 ALPEILFAKVSQGHNNLSLPRCTFSEQNOAETHAWFTSRFLYHAGFLLPMLVWGVCYVG 240
Qy 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Db 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
Qy 301 PVAITWCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Db 301 PVAITWCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 9

US-09-104-296-6
; Sequence 6, Application US/09104296
; Patent No. 6087475
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PP4A Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,296
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/810782
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0706P2C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-09-104-296-6

Query Match 100.0%; Score 1953; DB 3; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MNYPLTLEMDLENLEDLFWELDRDLNNDTSLVENHLCPCATGSLMASFKAVFPVAYSLL 60
Db 1 MNYPLTLEMDLENLEDLFWELDRDLNNDTSLVENHLCPCATGSLMASFKAVFPVAYSLL 60
Qy 61 IFELGVIGNVLVLILERHRQTRSTETFLFHLAVADLLLVILPFAVAGSVGVLGTF 120
Db 61 IFELGVIGNVLVLILERHRQTRSTETFLFHLAVADLLLVILPFAVAGSVGVLGTF 120
Qy 121 LCKTVIALHKVNFYCSSLLACIAVDRIYLAIVHAYHRRRLLSIHITCGTIWLVGFLL 180
Db 121 LCKTVIALHKVNFYCSSLLACIAVDRIYLAIVHAYHRRRLLSIHITCGTIWLVGFLL 180
Qy 181 ALPEILFAKVSQGHNNLSLPRCTFSEQNOAETHAWFTSRFLYHAGFLLPMLVWGVCYVG 240
Db 181 ALPEILFAKVSQGHNNLSLPRCTFSEQNOAETHAWFTSRFLYHAGFLLPMLVWGVCYVG 240
Qy 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFDLTLARLKAVDNTCKLNGSL 300
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Qy 301 PVAITWCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Db 301 PVAITWCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCOLPFSWRSSSL 360
Qy 361 SESENATSLTTF 372
Db 361 SESENATSLTTF 372

RESULT 10
US-08-982-493-8
; Sequence 8, Application US/08982493
; Patent No. 6110695
; GENERAL INFORMATION:
; APPLICANT: Gunn, Michael D
; APPLICANT: Williams, Lewis T
; APPLICANT: Cyster, Jason G
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
; TITLE OF INVENTION: Receptor Interactions
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,493
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCSFT98-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-992-493-8
Query Match 100.0%; Score 1953; DB 3; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
QY 61 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 61 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
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DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180
QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
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DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 11
US-09-170-496D-66
; Sequence 66, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 66
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-66
Query Match 100.0%; Score 1953; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 8.7e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
DB 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
QY 61 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 61 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180

QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRRSSL 360
DB 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372
RESULT 12
US-09-949-016-10255
; Sequence 10255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10255
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10255
Query Match 100.0%; Score 1953; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 8.9e-176;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 60
DB 7 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPMASFKAVFPVAYS 66
QY 61 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 120
DB 67 IFLLGVGNVLVILVILHRHQRTRSSSTETFLPHLAVADLLVFLPPFAVAEGSVGWLTGF 126
QY 121 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 180
DB 127 LCKTVIALHKVNFYCSSLLACIAVDRYLAIVHAVHAYRHRRLLSIHITCGTIWLVGFL 186
QY 181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 187 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 246
QY 241 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 300
DB 247 VVHRLQAQRPPQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNGSL 306
QY 301 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRRSSL 360
DB 307 PVAITWCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRRSSL 366
QY 361 SESENATSLTTF 372
DB 367 SESENATSLTTF 378

RESULT 13
US-09-170-496D-200
; Sequence 200, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170.496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-200

Query Match 99.7%; Score 1947; DB 4; Length 372;
Best Local Similarity 99.7%; Pred. No. 3.2e-175;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DB 61 IFLGVIGNVLVLILRHRQTRSTETFLHLAVADLLVFLPFAVAEGSVGWVLTGF 120
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DB 121 LCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLSIHITCGTILVGFLL 180
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DB 181 ALPEILPAKVSQGHNNLSLPRCTFQENOAETHAWFTSRFLYHVAGFLLPMLVGMWCVG 240
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DB 241 VVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNSL 300
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DB 301 PVAITMCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPWSRSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 14
US-08-982-493-6
; Sequence 6, Application US/08982493
; Patent No. 6110695
; GENERAL INFORMATION:
; APPLICANT: Gunn, Michael D
; APPLICANT: Williams, Lewis T
; APPLICANT: Cyster, Jason G
; TITLE OF INVENTION: Modulating B Lymphocyte Chemokine /
; TITLE OF INVENTION: Receptor Interactions
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA

ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,493
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCSFT98-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-982-493-6

Query Match 83.7%; Score 1635; DB 3; Length 374;
Best Local Similarity 82.9%; Pred. No. 7.5e-146;
Matches 310; Conservative 29; Mismatches 33; Indels 2; Gaps 1;
QY 1 MNYPLTLEMD--LENLEDFWELDRDNDYNTSLVENHLCPCATEGPMASFKAVFVPVAY 58
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QY 59 SLIFLGVIGNVLVLILRHRQTRSTETFLHLAVADLLVFLPFAVAEGSVGWVLTG 118
DB 61 SLIFLGVIGNVLVLILRHRQTRSTETFLHLAVADLLVFLPFAVAEGSVGWVLTG 120
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DB 121 TFLCKTVIALHKVNFVCSLLACIADRYLAIVHAYRHRRLSIHITCGTILVGF 180
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DB 181 LFALPEILPAKVSQGHNNLSLPRCTFQENOAETHAWFTSRFLYHVAGFLLPMLVGMWCV 240
QY 239 VGVVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG 298
DB 241 VGVVHRLQAQRPPQKAKRVAILVTSIFFLCWSPYHIVIFLDTLARLKAVDNTCKLNG 300
QY 299 SLPVAITMCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPWSR 358
DB 301 YLSVAITLCEFLGLAHCCCLNPMLYTPAGVKFRSDLSRLTLKLGCTGPASLCQLFPWN 360
QY 359 SLSESENATSLTTF 372
DB 361 SLSESENATSLTTF 374

RESULT 15
US-08-709-838-2
; Sequence 2, Application US/08709838
; Patent No. 6140064
; GENERAL INFORMATION:
; APPLICANT: Loetscher, Marcel
; APPLICANT: Moser, Bernhard
; TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
; TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USES THEREFOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA

Search completed: August 29, 2005, 23:58:34
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 29, 2005, 23:51:16 ; Search time 164 Seconds
(without alignments)
891.272 Million cell updates/sec

Title: US-10-666-689-6
Perfect score: 1953
Sequence: 1 MNYPTLEMDLENLEDFWE.....PSWRRSSLSSENATSLTTF 372

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Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1953	100.0	372	9	US-09-104-063-6
2	1953	100.0	372	14	US-10-251-385-66
3	1953	100.0	372	14	US-10-225-567A-60
4	1953	100.0	372	14	US-10-239-423-80
5	1953	100.0	372	15	US-10-666-689-6
6	1953	100.0	378	15	US-10-276-774-2243
7	1947	99.7	372	14	US-10-251-385-200
8	1938.5	99.3	371	20	US-11-021-951-154
9	635	32.5	368	14	US-10-251-385-20
10	635	32.5	368	14	US-10-225-567A-74
11	635	32.5	368	14	US-10-345-680-59
					Sequence 6, Appli
					Sequence 66, Appl
					Sequence 80, Appl
					Sequence 2243, Ap
					Sequence 200, App
					Sequence 154, App
					Sequence 20, Appl
					Sequence 74, Appl
					Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-09-104-063-6
; Sequence 6, Application US/09104063
; Patent No. US20020168356A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PFAA Receptors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/09/104,063
; FILING DATE: 24-June-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/701265
; FILING DATE: 22-Aug-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/664228
; FILING DATE: 06-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076093
; FILING DATE: 11-JUN-1993

Sequence 2, Appli
Sequence 78, Appli
Sequence 4, Appli
Sequence 752, App
Sequence 304, App
Sequence 34, Appli
Sequence 2, Appli
Sequence 155, App
Sequence 174, App
Sequence 6402, Ap
Sequence 517, App
Sequence 36, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appl
Sequence 882, App
Sequence 16, Appl
Sequence 386, App
Sequence 4, Appli
Sequence 25, Appl
Sequence 7, Appli
Sequence 2394, Ap
Sequence 29, Appl
Sequence 30, Appl
Sequence 34, Appl
Sequence 74, Appl
Sequence 68, Appl
Sequence 70, Appl

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/810782
;; FILING DATE: 19-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Love, Richard B.
;; REGISTRATION NUMBER: 34,659
;; REFERENCE/DOCKET NUMBER: P0706P2C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415/225-5530
;; TELEFAX: 415/952-9881
;; TELEX: 910/371-7168
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 372 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
US-09-104-063-6

Query Match 100.0%; Score 1953; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60
DB 1 MNYPLTLEMDLENLEDFWELDRLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVAYSL 60

QY 61 IFLLGVIGNVLVILERHQRTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120
DB 61 IFLLGVIGNVLVILERHQRTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAI VHAHVAYRHRLLSHITCGTILWVGFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAI VHAHVAYRHRLLSHITCGTILWVGFL 180

QY 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240
DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

QY 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300
DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 2
US-10-251-385-66
; Sequence 66, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Protein-Coupled
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-29
; PRIOR APPLICATION NUMBER: US/09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-251-385-66

Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAI VHAHVAYRHRLLSHITCGTILWVGFL 180

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DB 181 ALPEILPAKVSQGHNNSLPRCTFSQENQAETHAWFTSRFLYHVAGFLPMLVMGWCYVG 240

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DB 241 VVHRLQAQRPRQKAVRVAILVTSIFFLCWSPYHIVIFLDTLARKAVDNTCKLNGSL 300

QY 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360
DB 301 PVAITMCEFLGLAHCCCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSS 360

QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 3
US-10-225-567A-60
; Sequence 60, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Burner, Joseph P.
; APPLICANT: Brown, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPT
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-60

Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 IFLLGVIGNVLVILERHQRTRSSSTETFLFLAVADLLVFLPFAVAEGSVGVLTGF 120

QY 121 LCKTVIALHKVNFYCSSLLACIAVDYRLAI VHAHVAYRHRLLSHITCGTILWVGFL 180
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DB 301 PVAITMCEFLGLAHCCCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 4
US-10-239-423-80
; Sequence 80, Application US/10239423
; Publication No. US2003018689A1
; GENERAL INFORMATION:
; APPLICANT: FORSSMANN, Wolf-Georg; FORSSMANN, Ulf; ADERWANN, Knut;
; APPLICANT: HEITLAND, Aleksandra; SPODSBERG, Nikolaj
; TITLE OF INVENTION: Diagnostic Agent and Medicament for Examining the
; TITLE OF INVENTION: Cell Surface Proteome of Tumor and Inflammation Cells and
; TITLE OF INVENTION: For Treating Tumor Diseases and Inflammatory Diseases,
; TITLE OF INVENTION: Preferably with the Aid of Specific Chemokine
; TITLE OF INVENTION: Receptor Analysis and Chemokine Receptor/Ligand Interaction
; FILE REFERENCE: 02217us
; CURRENT APPLICATION NUMBER: US/10/239, 423
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: DE10016013.1
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 80
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Amino Acid Sequence for the Generation of Antibodies
US-10-239-423-80

Query Match 100.0%; Score 1953; DB 14; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPLMSPKAVFVPVAVSL 60
DB 1 MNPPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPLMSPKAVFVPVAVSL 60
QY 61 IFLGVGNVLVLILERHQRTRSTETFLHLAVADLLVLPFAVAEGSVGWVLTGF 120
DB 61 IFLGVGNVLVLILERHQRTRSTETFLHLAVADLLVLPFAVAEGSVGWVLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIADVRLAIHVAVHAYHRRLLSIHITCGTILVGVFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIADVRLAIHVAVHAYHRRLLSIHITCGTILVGVFL 180
QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
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QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 5
US-10-666-689-6
; Sequence 6, Application US/10666689
; Publication No. US20040037830A1
; GENERAL INFORMATION:
; APPLICANT: Lee, James
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Human FF4A Receptors, Nucleic Acid Encoding and
; TITLE OF INVENTION: Antibodies Binding Thereto
; FILE REFERENCE: P0706P2C2D2C1
; CURRENT APPLICATION NUMBER: US/10/666,689
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US 09/104,063
; PRIOR FILING DATE: 1988-06-24
; PRIOR APPLICATION NUMBER: US 08/701,265
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/664,228
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/076,093
; PRIOR FILING DATE: 1993-06-11
; PRIOR APPLICATION NUMBER: US 07/810,782
; PRIOR FILING DATE: 1991-12-19
; PRIOR APPLICATION NUMBER: US 07/677,211
; PRIOR FILING DATE: 1991-03-29
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-666-689-6

Query Match 100.0%; Score 1953; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPLMSPKAVFVPVAVSL 60
DB 1 MNPPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPLMSPKAVFVPVAVSL 60
QY 61 IFLGVGNVLVLILERHQRTRSTETFLHLAVADLLVLPFAVAEGSVGWVLTGF 120
DB 61 IFLGVGNVLVLILERHQRTRSTETFLHLAVADLLVLPFAVAEGSVGWVLTGF 120
QY 121 LCKTVIALHKVNFYCSSLLACIADVRLAIHVAVHAYHRRLLSIHITCGTILVGVFL 180
DB 121 LCKTVIALHKVNFYCSSLLACIADVRLAIHVAVHAYHRRLLSIHITCGTILVGVFL 180
QY 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
DB 181 ALPEILFAKVSQGHNNLSLPRCTFSQENQAETHAWFTSRFLYHVAGFLLPMLVMGWCYVG 240
QY 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
DB 241 VVHRLQAORRQOKAVRAVAILVTSIFFLCWSPYHIVIFLDTLRLKAVDNTCKLNGSL 300
QY 301 PVAITMCEFLGLAHCCCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
DB 301 PVAITMCEFLGLAHCCCLNPLMYTFAGVKFRSDLSRLTLKLGCTGPASLCQLPFSWRSSSL 360
QY 361 SESENATSLTTF 372
DB 361 SESENATSLTTF 372

RESULT 6
US-10-276-774-2243
; Sequence 2243, Application US/10276774
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/ Publication No. US20040053245A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc.
/ APPLICANT: Tang, Y. Tom et al
/ TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
/ FILE REFERENCE: 21272-030
/ CURRENT APPLICATION NUMBER: US/10/276,774
/ CURRENT FILING DATE: 2002-11-18
/ PRIOR APPLICATION NUMBER: 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 2700
/ SOFTWARE: Custom
/ SEQ ID NO 2243
/ LENGTH: 378
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-276-774-2243

Query Match      100.0%; Score 1953; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.6e-165;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSL 60
      |||||||
Db      7 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSL 66

QY      61 IFLLGVIGNVLVLILRHQTRSTETFLHLAVADLLVFLPFAVAGSGVWVLGTF 120
      |||||||
Db      67 IFLLGVIGNVLVLILRHQTRSTETFLHLAVADLLVFLPFAVAGSGVWVLGTF 126

QY      121 LCKTVIALHKVNFYCSLLACIAVDRLAIIVHAYHRRLLSHITCGTIWLVGFLL 180
      |||||||
Db      127 LCKTVIALHKVNFYCSLLACIAVDRLAIIVHAYHRRLLSHITCGTIWLVGFLL 186

QY      181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAMFTSRFLYHVAGFLPMLVMGWCYVG 240
      |||||||
Db      187 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAMFTSRFLYHVAGFLPMLVMGWCYVG 246

QY      241 VVHRLQAQRPRQKARVAIVLTSIFFLCWSPHYHIFDLTLARLKAVDNTCKLNGSL 300
      |||||||
Db      247 VVHRLQAQRPRQKARVAIVLTSIFFLCWSPHYHIFDLTLARLKAVDNTCKLNGSL 306

QY      301 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRRSSL 360
      |||||||
Db      307 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRRSSL 366

QY      361 SESENATSLTTF 372
      |||||||
Db      367 SESENATSLTTF 378

RESULT 7
US-10-251-385-200
/ Sequence 200, Application US/10251385
/ Publication No. US20030105292A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
/ TITLE OF INVENTION: Protein-Coupled
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: AREN-0040
/ CURRENT APPLICATION NUMBER: US/10/251,385
/ CURRENT FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: US/09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 200
/ LENGTH: 372
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-251-385-200

Query Match      99.7%; Score 1947; DB 14; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.4e-165;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSL 60
      |||||||
Db      1 MNYPLTLEMDLENLEDFWELDRDLDNYNDTSLVENHLCPCATEGPLMASFKAVFPVPVAYSL 60

QY      61 IFLLGVIGNVLVLILRHQTRSTETFLHLAVADLLVFLPFAVAGSGVWVLGTF 120
      |||||||
Db      61 IFLLGVIGNVLVLILRHQTRSTETFLHLAVADLLVFLPFAVAGSGVWVLGTF 120

QY      121 LCKTVIALHKVNFYCSLLACIAVDRLAIIVHAYHRRLLSHITCGTIWLVGFLL 180
      |||||||
Db      121 LCKTVIALHKVNFYCSLLACIAVDRLAIIVHAYHRRLLSHITCGTIWLVGFLL 180

QY      181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAMFTSRFLYHVAGFLPMLVMGWCYVG 240
      |||||||
Db      181 ALPEILFAKVSQGHNNSLPRCTFSQENQAETHAMFTSRFLYHVAGFLPMLVMGWCYVG 240

QY      241 VVHRLQAQRPRQKARVAIVLTSIFFLCWSPHYHIFDLTLARLKAVDNTCKLNGSL 300
      |||||||
Db      241 VVHRLQAQRPRQKARVAIVLTSIFFLCWSPHYHIFDLTLARLKAVDNTCKLNGSL 300

QY      301 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRRSSL 360
      |||||||
Db      301 PVAITWCEFLGLAHCLNPMLYTFAGVKFRSDLSRLTLKLGCTGPASLQOLPFSWRRSSL 360

QY      361 SESENATSLTTF 372
      |||||||
Db      361 SESENATSLTTF 372

RESULT 8
US-11-021-951-154
/ Sequence 154, Application US/11021951
/ Publication No. US20050175581A1
/ GENERAL INFORMATION:
/ APPLICANT: HAUPTS, Ulrich
/ APPLICANT: KOLTERMANN, Andre
/ APPLICANT: SCHEIDIG, Andreas
/ APPLICANT: VOTSMEIER, Christian
/ APPLICANT: Kettling, Ulrich
/ APPLICANT: COCO, Wayne Michael
/ TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
/ TITLE OF INVENTION: And Diagnostic Use Thereof
/ FILE REFERENCE: 04156.0002U5
/ CURRENT APPLICATION NUMBER: US/11/021,951
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: 10/872,198
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 60/543,518
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/524,960
/ PRIOR FILING DATE: 2003-11-25
/ PRIOR APPLICATION NUMBER: EP 04003058
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: EP 03025871
/ PRIOR FILING DATE: 2003-11-11
/ PRIOR APPLICATION NUMBER: EP 03025851
/ PRIOR FILING DATE: 2003-11-10
/ PRIOR APPLICATION NUMBER: EP 03013819
/ PRIOR FILING DATE: 2003-06-18
/ NUMBER OF SEQ ID NOS: 191
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 154
/ LENGTH: 371
/ TYPE: PRT
/ ORGANISM: Homo sapiens
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Venkateswarlu, Karicheti
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING 34021, 44099, 25278,
TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 62553, 302, 323,
TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
FILE REFERENCE: ME102-012P1RNM-OMNI
CURRENT APPLICATION NUMBER: US/10/345,680
CURRENT FILING DATE: 2003-01-16
PRIORITY FILING DATE: 2003-01-16
PRIORITY FILING DATE: 2002-01-18
PRIORITY FILING DATE: 2002-02-28
PRIORITY FILING DATE: 2002-03-15
PRIORITY FILING DATE: 2002-04-19
PRIORITY FILING DATE: 2002-08-14
PRIORITY FILING DATE: 2002-09-27
PRIORITY FILING DATE: 2002-10-21
PRIORITY FILING DATE: 2002-11-05
PRIORITY FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 66
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 368
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-345-680-59

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
QY 11 LENLEDFWELDRDNYNDTSVLVNHLCPCATEGPMASFKAVFVPVAVYSLIIFLLGVIGNV 70
Db 20 LENFSSSY---DYGENESD-SCTSPPCPO---DFSINFDRAFLPALYSLLFLGLLNG 72
QY 71 LVLVILHRHQTRSTETFLHLAVADLLVFLPFAVAGSVGWLGTFLCKTVIALHK 130
Db 73 AVAAVLLSRRTALSSDTDFLLHLAVADTLVLVTLPLWADAAVQWVFGSLCKVAGALFN 132
QY 131 VNFYCSLLLACIAVDYRLAIVHAVYHRHRLLSIHTCGTITWLVGFLALPEILFAKV 190
Db 133 INFYAGALLLACISFDYRLINIVHATQLYRRGPPARVTLTCLAVGCLLFLALPDFL-- 190
QY 191 SOGHHNSL--PRCTSQENQAETHAWFTSRFLYHVAGFLPMLVMGVCVGVVHRLROA 248
Db 191 -SAHDERLNATHCQYNFPQVGR-----ALRVQLVAGFLPLVMAYCYAHILAVL-LV 244
QY 249 QRRPQROKAVRAVAILVTSIFFLCWSPHYIVIFLDTLARKAVDNTCKLNGSLPVAITMCE 308
Db 245 SRGQRLRANRLVTVVAVAFALCWTPTVHLVVDILMDLGALARNCGRESKVDVAKSVTS 304
QY 309 FLGLAHCCNPMLYTFAGVFKPRSDLSRLITKLGCTGPASLCQLFPFWR--SSLSSEENAT 367
Db 305 GLGYMHCCNPLLYAFVGVKFRERMMWMLLLRLGCPNQRGLQRPSSRRSSWSETSEAS 364

RESULT 12
US-10-251-686-2
Sequence 2, Application US/10251686
Publication No. US20030158392A1
GENERAL INFORMATION:
APPLICANT: Loescher, Marcel
Moser, Bernhard
Qin, Shixin
Mackay, Charles R.

TITLE OF INVENTION: IP-10/MIG RECEPTOR DESIGNATED CXCR3,
ANTIBODIES, NUCLEIC ACIDS, AND METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/251,686
FILING DATE: 20-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/829,839
FILING DATE: 31-MAR-1997
APPLICATION NUMBER: US 08/709,838
FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: TKI96-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-251-686-2

Query Match 32.5%; Score 635; DB 14; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;
QY 11 LENLEDFWELDRDNYNDTSVLVNHLCPCATEGPMASFKAVFVPVAVYSLIIFLLGVIGNV 70
Db 20 LENFSSSY---DYGENESD-SCTSPPCPO---DFSINFDRAFLPALYSLLFLGLLNG 72
QY 71 LVLVILHRHQTRSTETFLHLAVADLLVFLPFAVAGSVGWLGTFLCKTVIALHK 130
Db 73 AVAAVLLSRRTALSSDTDFLLHLAVADTLVLVTLPLWADAAVQWVFGSLCKVAGALFN 132
QY 131 VNFYCSLLLACIAVDYRLAIVHAVYHRHRLLSIHTCGTITWLVGFLALPEILFAKV 190
Db 133 INFYAGALLLACISFDYRLINIVHATQLYRRGPPARVTLTCLAVGCLLFLALPDFL-- 190
QY 191 SOGHHNSL--PRCTSQENQAETHAWFTSRFLYHVAGFLPMLVMGVCVGVVHRLROA 248
Db 191 -SAHDERLNATHCQYNFPQVGR-----ALRVQLVAGFLPLVMAYCYAHILAVL-LV 244
QY 249 QRRPQROKAVRAVAILVTSIFFLCWSPHYIVIFLDTLARKAVDNTCKLNGSLPVAITMCE 308
Db 245 SRGQRLRANRLVTVVAVAFALCWTPTVHLVVDILMDLGALARNCGRESKVDVAKSVTS 304
QY 309 FLGLAHCCNPMLYTFAGVFKPRSDLSRLITKLGCTGPASLCQLFPFWR--SSLSSEENAT 367
Db 305 GLGYMHCCNPLLYAFVGVKFRERMMWMLLLRLGCPNQRGLQRPSSRRSSWSETSEAS 364

RESULT 13
US-10-239-423-78
Sequence 78, Application US/10239423
Publication No. US2003018689A1


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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 752
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-752

Query Match      32.5%; Score 635; DB 15; Length 368;
Best Local Similarity 40.8%; Pred. No. 4.2e-48;
Matches 147; Conservative 50; Mismatches 145; Indels 18; Gaps 8;

QY 11 LENLEDFWELDRIDNDTSLVENHLCPCATEGPLMASFKAVFVPVAYSILIFLLGVIGNV 70
Db 20 LENFSSSY--DYGENESD-SCCTSPCPQ---DFSINFDRAFLPALYSLLFLGLGNG 72

QY 71 LVLVILERHROTBSSTETFLHLAVADLLAVFILPPAVAESGVGWLGTFLCKVTIALHK 130
Db 73 AVAAVLLSRRTALSSDTFLHLAVADTLLVLTPLWADVAVQWVFGSLCKVAGALFN 132

QY 131 VNFYCSLLIACIADRYLAIHAVHAYRHRRLLSIHITCGTIWLVGFLIALPEILFAKV 190
Db 133 INFYAGALLACISFDEYLNIVHATQLYRRGPPARVTLTCLAVWGLCLLEALPDFIFL-- 190

QY 191 SQGHNNSL--PRCTFSQENQAEATHWFTSRFLYHVAGFLLPMLVGMWCYGVGVHRLROA 248
Db 191 -SAHDERLNATHCQYNFPQVGRT---ALRVLQVLVAGFLLPLLVMAICYAHILAVL-LV 244

QY 249 QRRPQOKAVRVAILYTSIFFLCWSPVHIVIFLDTLRLKAVDNTCKLNGSLPVAITMCE 308
Db 245 SRGQRLRAWLVVVVVVAFALCWTYPVHLVVLVDILMDLGALRNCGRSRRVDVAKSVTS 304

QY 309 FLGLAHCCLNPMPLYTFAGVKFRSDLSRLLTKLCTGTPASLCQLFPSPWRR--SSLSESENAT 367
Db 305 GLGYMHCCLNPLLYAFVGVKFRERMMWMLLRGLGCPNQRGLQRPSSRRRDSWSETSEAS 364
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Search completed: August 30, 2005, 00:01:24
Job time : 166 secs